

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 6, 2005, 00:35:15 ; Search time 11362 Seconds  
(without alignments)  
12452.463 Million cell updates/sec

Title: US-10-692-556-1

Perfect score: 3717

Sequence: 1 atgttttgccgcggcggg.....ccttgatacttagcatga 3717

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_est3:\*

4: gb\_est4:\*

5: gb\_est5:\*

6: gb\_est6:\*

7: gb\_est7:\*

8: gb\_gse1:\*

9: gb\_gse2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	146	3.9	689	AG126971	Pan trogl
C 2	124.2	3.3	650	AG061486	AG061486 Pan trogl
C 3	123.4	3.3	673	AG131496	AG131496 Pan trogl
C 4	95.4	2.6	706	AG049882	AG049882 Pan trogl
C 5	90.4	2.4	645	AJ723867	AJ723867 Pan trogl
6	89	2.4	724	BG826841	BG826841 602750915
7	89	2.4	1038	BX382861	BX382861 601058865
8	86.4	2.3	503	BE535321	BE535321 601058865
C 9	85.4	2.3	925	BX350425	BX350425 EX350425
10	84.8	2.3	1368	BQ053856	BQ053856 AGENCOURT
11	84.6	2.3	687	B1118205	B1118205 602867491
C 12	84.2	2.3	727	AJ723868	AJ723868 AJ723868
C 13	82.2	2.2	1956	CG754548	CG754548 P050-1-A1
14	82	2.2	453	BP096735	BP096735 BP096735
15	81.6	2.2	1009	CNS010EM	CNS010EM Drosophil
16	81.2	2.2	822	BQ743697	BQ743697 WHE4107 C
17	79.8	2.1	347	CK234399	CK234399 SB0100060
18	79.8	2.1	834	BE737103	BE737103 601304437
19	77.4	2.1	1035	BQ071299	BQ071299 AGENCOURT
20	76.4	2.1	917	CR633636	CR633636 Tetraodon
21	76.4	2.1	1398	CR716960	CR716960 Tetraodon
22	75.4	2.0	462	B1344718	B1344718 373258 MA
23	75.4	2.0	1083	CK206171	CK206171 FGA501775
24	74.8	2.0	998	BQ881418	BQ881418 AGENCOURT

25	74.6	2.0	541	2	BE013096	BE013096 122887 MA
C 26	74.4	2.0	925	9	CNS00091P	AL051013 Drosophil
27	73.6	2.0	581	4	BG145187	BG145187 uc76909.y
28	73.6	2.0	712	6	CD372246	CD372246 UI-R-GOO-
29	73.6	2.0	923	5	BUS14091	BUS14091 AGENCOURT
30	73.6	2.0	3409	3	AK088310	AK088310 Mus muscu
31	73.4	2.0	568	2	BF203965	BF203965 601868975
32	73.4	2.0	788	2	BF205093	BF205093 601868975
C 33	73.2	2.0	1628	9	CG757066	CG757066 P052-2-A0
34	72.8	2.0	925	9	CNS00091P	AL053013 Drosophil
C 35	72.6	2.0	699	9	BX906960	BX906960 Leishmani
C 36	72.6	2.0	699	9	LBAF026G07	BX544067 Leishmani
C 37	72.6	2.0	684	8	AQ163340	AQ163340 mgxb0023L
38	71.2	1.9	371	2	BF292456	BF292456 WHE2214 A
39	71.2	1.9	953	5	BQ232039	BQ232039 AGENCOURT
40	70.6	1.9	1509	9	CL959255	CL959255 OsIFCC002
C 41	70	1.9	1002	9	AG046242	AG046242 Pan trogl
42	69.6	1.9	798	4	BM044191	BM044191 603621433
43	69.6	1.9	876	4	BM048573	BM048573 603623915
44	69.4	1.9	699	6	CD371733	CD371733 UI-R-GOO-
C 45	69	1.9	935	9	CNS0065XK	AL066051 Drosophil

## ALIGNMENTS

RESULT 1  
AG126971/c  
LOCUS AG126971  
DEFINITION Pan troglodytes DNA, clone: PTB-137L02.F, genomic survey sequence.  
ACCESSION AG126971  
VERSION AG126971.1 GI:16656136  
KEYWORDS GSS  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
REFERENCE 1  
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
TITLE BAC end sequences of Library PTB  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 689)  
AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
TITLE Direct Submission  
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail:chimbesc@sc.riken.go.jp, Fax:81-45-503-9170)  
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.  
PRIMERS  
Sequencing: -21m13  
LIBRARY Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI.  
Location/Qualifiers  
1. 689  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="PTB-137L02.F"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC Library"

Query Match 3.9%; Score 146; DB 9; Length 689;  
Best Local Similarity 57.5%; Pred. No. 7.8e-18;

Matches 320; Conservative 0; Mismatches 231; Indels 6; Gaps 3;

QY 2325 CTTGCTGAGCATCTGCTGGCGCATGCTGGTGGCCATGCGAAAGCAGATCCGCTCGCGAT 2384

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 628 CTTCTGGCTAGTCTGTTGACCTCTGCTGGTGGCCAAAGCGCAAGGCATCAAGAGCTGCT 569

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 2385 CCC--CCAGAGCACCCCGAGGAGCGCTCTCTCGACACGACACAGCGGCCCATCAAG 2442

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 568 GNGCGCCTGGCGAGATCCGCGCCAAAGACCATCTCTCGAAGACGACGCTGGCCATCAAG 509

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 2443 GTGTGTGCAACTCGGTGTACGGGTTCACCGGGCGCAGCAGCGTCTCTGCGCCCTGCGCTG 2502

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 508 TGCACTGCAAGCGCGTCTACGGCTTCACGGGTGCG--CAAGCGCTCTTCTCCCTGCGCTC 450

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 2503 CACGTGGCGCCACCGTGCAGACACCATTCGCGCGCGAGATGCTCTCGCAACGCGCGGTAC 2562

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 449 TCCATCGCGAGACGCTGACGCTGCAGGCGCGCACGATGTTGGAGCGGCCAAGGCGCTTC 390

QY 2563 GTGCAGCGCGCTGGCGGAGTTGATCAGCTGCTGGCGGACTTTCGCGAGCGCGCGCGC 2622

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 389 GTGGAGGCGCTGAGCGCCCGCAACCTGCAGGCGCTGGCGCCCTCTCCCGAGCGCTGGGCG 330

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 2623 ATGCGCGCCCGCGTCTGCTTCCATGCGCATCATCTACGGGACACGGAATCCATTTTC 2682

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 329 CCCCTCAACCCG---AGGGCAGCTTCGAGTCATCTACGGGACACGACTCGCTGTTT 273

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 2683 GTTTTGTGCGCGGCGCTCACGGCGCGGCGCTGTGGCCATGGGCGCAAGATGCGGAGC 2742

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 272 ATCGAGTCCGGGGGTTTTCAGAGAGCGAGACCCCTGCGCTTTCGCGATGCGCTGGCGGCC 213

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 212 CACACACCGGAGCGCTGTTGTGCGCCCGCATCTCCCTGGAGGCGGAGAACCTTCTCC 153

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 2803 AAGCTGCTGCTCATGCCCAAGAAAGTACATCGCGCTCATCTGCGGGGCAAGATGCTC 2862

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 152 TGCTGTGCTGATTACAAAGAGAGATATGTGGGGTGCTGACGAGCGGCAAGACCTG 93

QY 2863 ATCAAGGCGGTGGATCT 2879

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 92 ATGAAGGGGGTGGAGCT 76

RESULT 2

AG061486/c

LOCUS AG061486 650 bp DNA linear GSS 03-NOV-2001

DEFINITION Pan troglodytes DNA, clone: PTB-049119.R, genomic survey sequence.

ACCESSION AG061486

VERSION AG061486.1 GI:16613288

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Tokoki,Y., Watanabe,H. and Sakaki,Y.

TITLE BAC end sequences of Library PTB

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 650)

1 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Tokoki,Y., Watanabe,H. and Sakaki,Y.

2 Direct Submission

TITLE Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimbese@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

JOURNAL Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

COMMENT PRIMERS

Sequencing: M13Rev

LIBRARY

Vector : pKS145

R.Site 1 : SacI

R.Site 2 : SacI

FEATURES

Location/Qualifiers

1..650

/organism="pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

/clone="PTB-049119.R"

/sex="male"

/cell\_type="lymphoblast"

/clone\_lib="PTB Chimpanzee Male BAC Library"

ORIGIN

Query Match 3.3%; Score 124.2; DB 9; Length 650;

Best Local Similarity 53.4%; Pred. No. 1.3e-13;

Matches 306; Conservative 0; Mismatches 263; Indels 4; Gaps 2;

QY 2491 CTGCCCTGCTGCAAGTGGCGCCACCGTGACGACCATCGGCGCGGAGATGCTCTCGCG 2550

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 650 CTTCCCTGCTAGCATCATCCGAGACGTAACGCTGCAGGCGCCGACTATGTTGTAGCGG 591

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 2551 ACGCGCGGTACGTCAGCGCGCTGGCGGAGTTTCGATCAGCTGCTGGCGACTTTCCG 2610

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 590 GCCAAGGCTTCGTGGAGACCCCTGAGCCCCCACCCTGACGAGCCCTGGCGCCCTCCCCG 531

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 2611 GAGCGCGCGGCATGCGCGCCCGCTCGTACCTTCATTCGCGCATCATCTACGGGACACG 2670

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 530 GAGCGCTGGCGCCCTCAACCCG---AGGGCAGCTTCGAGTCATCTACGGGACACG 474

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 2671 GACTCCATTTTGTGTCGCGGCGCTCACGGCGCGGCGCTGTGGCCATGCGCGAC 2730

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 473 GACTCGCTGTTATCGAGTGGCGGGGTTTTCAGAGAGCGAGACCCCTGCGCTTTGCCGAT 414

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 2731 AAGATGGCGAGCCACATCTCGCGCGCTGCTTCTCTCCCGCATCAAGCTCGAGTGCGAA 2790

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 413 GCCTGGCGGCCACACACCCGAGCGCTGTTGTGGCCCCCATCTCCCTGTAGGCGAG 354

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 2791 AAAAGCTTCAACAGCTGCTCTCATCGCCAAAGAAAGTACATCGGCGCTCATCTGCGG 2850

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 353 AAGACCTTGTCTGCTGATGCTATTACAAAGAGATATGTGGGGGTGCTGACGAG 294

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 2851 GGCAAGATGCTCATCAAGGCGTGGATCTGTGGCGCAAAACACTGGCGCTTATCAAC 2910

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 293 GGCAAGACCCCTGATGAAGGGGGTGGAGCTCGTCCGGAAGACGGCTCGAAGTTGTGCAG 234

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 2911 CGCACCTCCAGGCGCTGCTGACCTGCTG---TTTTACGACGATACCGTATCCGAGCGGC 2969

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 233 ACACGCTGCGCGCGCTGCTGACCTGCTGTGACAGGATCCCGGGTAAAGGAGGCGGC 174

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 2970 CGCGCGTTAGCGAGCGCCCGCAGAGGAGTGGCTGGCGGACCCCTGCGCGAGGAGTACT 3029

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 173 CAGCTCTCTCTCCACCGGCCCTTCCAAGAGTCAATTTACACAAGGGCTACCTGTGGGCTT 114

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 3030 GCAGCGTTGGCGCGCTCTCTGCTAGACGCGCA 3062

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 113 TTTGCCGCTCATGACATCCTCTAAACACGCGCTA 81

Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3

AG131496/c

LOCUS AG131496 673 bp DNA linear GSS 04-NOV-2001

DEFINITION Pan troglodytes DNA, clone: PTB-143J08.R, genomic survey sequence.

ACCESSION AG131496

VERSION AG131496.1 GI:16661174

KEYWORDS GSS.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,

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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
REFERENCE
2 (bases 1 to 673)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
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/sex="male"
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/clone_lib="PTB Chimpanzee Male BAC Library"
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Best Local Similarity 56.2%; Pred. No. 1.8e-13;
Matches 232; Conservative 0; Mismatches 181; Indels 0; Gaps 0;
QY 2650 CGCATCATCTACGGGACACGACCTCATTTTGTGTCGGCGCTCATCGCGCGG 2709
Db |||||
QY 518 CGAGTCATGTACGGGACACGACCTCTCTGTTATCGATGGCGGGGTTTTCAGAGAGC 459
Db |||||
QY 2710 GGCCTGGTGGCCATGGGCGACAGATGGCGAGCCATCTCGCGCGCGTGTCTCC 2769
Db |||||
QY 458 GAGACCTCGCTGGCGCATGCGTGGCGGCCACACCGCGAGCGCTGTTGTCGCGC 399
Db |||||
QY 2770 CCGATCAAGCTCGAGTGCAGAAACAGTTTCCACCAAGCTGCTCATCGCCCAAGAAAG 2829
Db |||||
QY 398 CCATCTCGCTGGAGCCGAGAGACCTTCTCTGCTGATGCTGATTACAAAGAGAGA 339
Db |||||
QY 2830 TACATCGGCGTTCATTCGGGGGCGAAGTGTCTCATCAAGGGCGTGGATCTGGTGGCGCAA 2889
Db |||||
QY 338 TATGTGGGGTGTCTGACGAGCGGACAGACCTGTATGAAGGGGTGGAGCTGTCGCGAAG 279
Db |||||
QY 2890 AACAACTGGCGTTTATCAACCGACCTTCAGGGCGCTGCTGACCTGCTGTTTACGAC 2949
Db |||||
QY 278 ACGGCTGCAAGTTTGTGCAGACACGCTGCGCGCGCTGCTGACCTGCTGTCGCGGAT 219
Db |||||
QY 2950 GATACCGTATCCGGAGCGCGCCCGCTTTCAGCGAGCGCCCGCAGAGAGTGGCTGGCG 3009
Db |||||
QY 218 GCCCGGTAAAGAGCGCGCCAGCTCTCTCCACCGGCCCTTCCAGAGTCATTATCA 159
Db |||||
QY 3010 CGACCCCTGCGCGAGGAGCTGAGGCGTTTCGGGGCGCTCTCGTAGAGCGCCCA 3062
Db |||||
QY 158 CAAGGGCTACCTGTGGGCTTTTGGCCGTCATTGACATCTTAACACGAGCCCTA 106
Db |||||

RESULT 4
AG049882/c 706 bp DNA linear GSS 02-NOV-2001
LOCUS Pan troglodytes DNA, clone: PTB-030C07.R, genomic survey sequence.
DEFINITION
ACCESSION AG049882
VERSION AG049882.1 GI:16586774
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
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Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
1  
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
BAC end sequences of Library PTB  
Unpublished  
2 (bases 1 to 706)  
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
Totoki,Y., Watanabe,H. and Sakaki,Y.  
Direct Submission  
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail:chimpes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,  
Tel:81-45-503-9111, Fax:81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB This BAC end  
was generated during the R&D process and may have higher chance of  
clone tracking errors.  
PRIMERS  
Sequencing: M13Rev  
LIBRARY  
Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI.  
Location/Qualifiers  
1..706  
/organism="Pan troglodytes"  
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/clone="PTB-030C07.R"  
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Query Match 2.6%; Score 95.4; DB 9; Length 706;  
Best Local Similarity 53.1%; Pred. No. 4.7e-08;  
Matches 249; Conservative 0; Mismatches 216; Indels 4; Gaps 2;  
QY 2412 CTTCTCTGACAGCAACGAGCGCGCATCAAGTGGTGTGCAACTCGGTGTACGGGTTCAC 2471  
Db |||||  
QY 580 CATCCATTTCAAACAACAGTTGACCATCAAGTGCAGTGCATCGCGTAATCGGTTTCAC 521  
Db |||||  
QY 2472 CGGGCGGACAGCGTCTTCTGCTGCTGCACTGGCGCGCCACCGTGACACCAATCGG 2531  
Db |||||  
QY 520 CGGGGTGGCCAAACGCGCTTTTCCCTCTGACCAATTATCAAGTTGGTAACTTTGCAGGT 461  
Db |||||  
QY 2532 CCGCG-AGATGCTCTCGCGACGCGGTAGTGCACGCGCGCTGGCGGAGTTTCGATC 2590  
Db |||||  
QY 460 CGCTTATATGTTGGAGCGGACCAAGGCTTCTGTAAGTCCATAAACCCCGCAACTTCG 401  
Db |||||  
QY 2591 AGTGTGCGCGACTTTTCGGAGGCGCGCGCATGCGGCGCCCGCGTCCGTACTCCATGC 2650  
Db |||||  
QY 400 AGGCTTGGCCCTCCCGTACGTTTGGCGCGCTCATCACCGA---GGGCCAGCTTT 344  
Db |||||  
QY 2651 GCATCATCTAGGGAGACGGAATCCATTTTGTGTTGTCGCGCGCTCAGCGCGCGG 2710  
Db |||||  
QY 343 GAGTCATATACGGGAACACGTACTCACTGTTTATTTAGTGGCGGGGTTTTCAGAGAACG 284  
Db |||||  
QY 2711 GCCTGGTGGCATGGCGCAAGAATGGCGAGCCACATCTCGCGCGCTGTTCTCCGCC 2770  
Db |||||  
QY 283 AGACCTGGCTTGGCAATGCCCTGTCCGCCACACCCCGAGCTTGTGTGGGCC 224  
Db |||||  
QY 2771 CGATCAAGCTCGAGTGCAGAAACAGTTTCAACAAGCTGCTCATGCCCAAGAAAAAGT 2830  
Db |||||  
QY 223 CCATCTCCCTGAAGACCGAGAAGACCTTCTCTGCTGATCTGATTACAAAGAGAGAT 164  
Db |||||  
QY 2831 ACATCGGCGTCTATCTGCGGGGCGAAGATGCTCATCAAGGGCGTGGATCT. 2879  
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QY 163 ATGTGGGGGTGCTGACGAGCGCAAGACCTGATTAAAGGGGTGTAGCT 115  
Db |||||

RESULT 5	AJ723867	645 bp	mRNA	linear	EST 07-OCT-2004
LOCUS	AJ723867	riken1	Gallus gallus	cdna clone 26j22s4	mRNA sequence.
DEFINITION	AJ723867				
ACCESSION	AJ723867				
VERSION	AJ723867.1	GI:53889281			
KEYWORDS	Est.				
SOURCE	Gallus gallus (chicken)				
ORGANISM	Gallus gallus				
REFERENCE					
AUTHORS	Caldwell,R.B., Kierzek,A.M., Arakawa,H., Bezzubov,Y., Zaim,J., Fiedler,P., Kutter,S., Blagodatki,A., Kostovska,D., Koter,M., Plachy,J., Carninci,P., Hayashizaki,Y. and Buerstedde,J.M.				
TITLE	Full-length cDNAs from bursal lymphocytes to facilitate gene function analysis				
JOURNAL	Unpublished (2004)				
COMMENT	Contact: Caldwell RB				
FEATURES	GSF - Forschungszentrum, Institut fuer Molekulare Strahlenbiologie Ingolstaedter Landstr. 1, D-85764 Neuherberg, GERMANY.				
source	Location/Qualifiers				
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	/db_xref="taxon:9031"				
	/clone="26j22s4"				
	/cell_type="bursal lymphocyte"				
	/dev_stage="2-3 weeks old"				
	/clone_lib="riken1"				
	/note="CB inbred strain"				
ORIGIN					
	Query Match	2.4%	Score 90.4;	DB 1;	Length 645;
	Best Local Similarity	50.2%	Pred. No. 4.4e-07;		
	Matches 254;	Conservative 0;	Mismatches 246;	Indels 6;	Gaps 1;
Qy	2116	GACCCACCTCCCGGTTTCACGTGACCCCGTGGTGTGTTGACTTTCACCGACCTGTAC	2175		
Db	645	GAGCCCAAGAAGGGTTACTACGAGTCCCCCATCGCACGTTGGACTTCAGCTCTCTGTAC	586		
Qy	2176	CCGACATCATCAGGCGGACACCTGTGCTTCAGTACGCTCTCCCTCGCGGCCGAGGCC	2235		
Db	585	CCCTCCATTATGATGGCCCAATCTGTGTACACCACTCTGTGCGCGCCGCGCGCG	526		
Qy	2236	GTGCGCACCTGAGGCGGACCGGACTACTTGAGATCGAGTGGGGGCCACGCGCTG	2295		
Db	525	CAGGCTACGGGCTGAGCCCCACGAATTATCCGACACCCACGGGGAT-----CTC	472		
Qy	2296	TTCTTCGTGAAGGCCACGTACGCGAGAGCTCTGTGAGCATCTCTGTGCGCATCGCTG	2355		
Db	471	TTTGTGACGGCGCGTGCCTGGGCTGTGCTCCCGCATCTCTCGAGGGGCTGTGGCG	412		
Qy	2356	GCCATCGGAAGCAGATCCGCTCGCGATCCCCAGAGACCCCGAGGAGGCGGTCCTC	2415		
Db	411	GCGCGGCGCAGGCGGAAGAGGAGCTGTCCGGGAGACGACCCGTTCCGGCGTCATGTC	352		
Qy	2416	CTCGACAAGCAACAGGCGGCATCAAGTGGTGTGCAACTCGGTGTACGGGTTTCACGGG	2475		
Db	351	CTGACGCGCGGAGATGGCGCTCAAGTCAGCGCCCACTCCGTGTACGGCTTCA CGGG	292		
Qy	2476	GCGCAGACGGTCTTCTGCGCTGCTGCAAGTGGCGGCCACCGTGCAGCACCATTCGGCGCG	2535		
Db	291	GCGCAGCGGGCGGCTGCGCTCGAGATCTCGCAGACGCTGACGGGTTTCGGCGCG	232		
Qy	2536	GAGATGCTCTCGGACGCGCGGTACGTGCACGCGCTGGGCGGAGTTTCGATCAGCTG	2595		
Db	231	CAGATGATCAGCGCACGACGAATTGGTGAGTTCGCACCTTCTGTGTGGCAATGGGTAC	172		
Qy	2596	CTGCGCGACTTTCGGAGGCGGCGG 2621			



QY 2339 TGTGTGCGCACTGGTGGCCATGCGAAACAGATCCGCTCGCGGATCCGCCAGAGCAC-- 2396  
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Db 306 TCTGAGAACTGTCTAGTGCCTCGGAGAGGCCAAGCCGAGCTGGCCAGGAGACAG 365  
| | | | |  
QY 2397 -CCCGAGAGGCGCTCTCTCGACAGACAGACAGCCGCCATCAAGTGGTGTGCAACT 2455  
| | | | |  
Db 366 ACCCTCTCGGCGCAGGTCTCTGGATGGAGCGGAGCTGCGCTGAAGGTGAGCGCAACT 425  
| | | | |  
QY 2456 CGGTGTACGGGTTCACCGGGGCGCAGCAGCGTCTTCTGCGCTGCTGCTGCACTGGCGGCCA 2515  
| | | | |  
Db 426 CGGTATACGGCTTCACTGGCGCCAGGTGGGCAAGTGGCGTGGCTGGAGATCTACAGA 485  
| | | | |  
QY 2516 CGGTGACGACCAATCGCGCGCGAGATGCTC 2544  
| | | | |  
Db 486 GCGTCACGGGTTCGACCTCAGATGATC 514  
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## RESULT 7

LOCUS BX382861  
DEFINITION Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED  
ACCESSION Homo sapiens cDNA clone CS0DJ001YC08 5-PRIME, mRNA sequence.  
VERSION BX382861  
KEYWORDS BX382861.2 GI:46833596  
SOURCE EST.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE Li.W.B., Gruber,C., Jessee,J. and Polayes,D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)  
COMMENT On May 8, 2003 this sequence version replaced gi:30459096.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
9280.f

For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0DJ001BB04QPl&c=9280.f.

## FEATURES

source  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DJ001YC08"  
/cell\_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"  
/cell\_line="JURKAT"  
/clone\_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 2.4%; Score 89; DB 5; Length 1038;  
Best Local Similarity 51.5%; Pred. No. 8.2e-07;  
Matches 262; Conservative 0; Mismatches 235; Indels 12; Gaps 2;  
QY 2039 AGGACGGGACGAGCGGAGGAGTGGCGCGAGACCGGGCGCGGACGTTGGGTACC 2098  
| | | | |  
Db 172 AGGCCATGACGAGGGGCTGTGATGCCCGTGTGAATGTCAGAGGCGCGGAGGACTACA 231  
| | | | |  
QY 2099 AGGGGGCGGGTCTCGACCCACCTCGGGTTTCAGTCGACCCCGTGGTGGTTTG 2158  
| | | | |  
Db 232 CGGGAGCGACTGTCTATCGAGGCCCTCAAAGGGTACTACGACGTGCCCATCGCCCTGG 291  
| | | | |

QY 2159 ACTTTGCCAGCGCTGTATCCAGCATCATCCAGGCCCAACACTGTGCTTCACTAGCTCT 2218  
| | | | |  
Db 292 ACTTCTCTCGCTGTATCCCGTCCATCATGATGGCCCAACACTGTGTTACACAGCTCC 351  
| | | | |  
QY 2219 CCCTCGGGCCGAGCGCTGCGCACCTGGAGCGGACACGGGACTACCTGGAGATGAGG 2278  
| | | | |  
Db 352 TTCCGC-----CCGGGACTGCACAGAACTGGGCTGACTGAGGATCAGTTTCATCA 402  
| | | | |  
QY 2279 TGGGGGGCGGAGCGGTGTTCTTCGTGAAGGCCACGATAGCGGAGCGCTGTGAGCATCC 2338  
| | | | |  
Db 403 GACCCCCACCGGGGACGAGTTTGTGAAGACCTCAGTGGGAAGGGGTGCTGCCCCAGA 462  
| | | | |  
QY 2339 TGCTGCGCACTGGCTGGCCATGCGAAAGCAGATCCGCTCGCGGATCCCCCAGAGCAC-- 2396  
| | | | |  
Db 463 TCCTGGAGAACCTGCTCAGTGCCTCGGAGAGGGCCAGGCCGAGCTGGCCAGGAGACAG 522  
| | | | |  
QY 2397 -CCCGAGAGGCGCTCTCTCTCGACAAGCAACAGCGCGCCATCAAGTGGTGTGCAACT 2455  
| | | | |  
Db 523 ACCCTCTCGGTGCCAGGTCTCTGGATGGACGGCAGCTGCGCTGAAGGTGAGCGCAACT 582  
| | | | |  
QY 2456 CGGTGTACGGGTTCACCGGGGCGGAGCAGCGTCTTCTGCGCTGCTGCGAGTGGCGCCA 2515  
| | | | |  
Db 583 CGGTATACGGCTTCACTGCGCGCCAGGTGGGCAAGTTGCCGTGGAGATCTCACAGA 642  
| | | | |  
QY 2516 CCGTGACGACCATCGCGCGCGAGATGCTC 2544  
| | | | |  
Db 643 GCGTCACGGGTTCGAGCTCAGATGATC 671  
| | | | |

## RESULT 8

LOCUS BE535321  
DEFINITION 601058865F1 NIH\_MGC\_10 Homo sapiens cDNA clone IMAGE:3445168 5',  
mRNA sequence.  
ACCESSION BE535321  
VERSION BE535321.1 GI:9763966  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/  
AUTHORS 1 (bases 1 to 503)  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Incyte Genomics, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM8415 row: b column: 17  
High quality sequence stop: 503.  
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/cell\_line="MGC36"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_10"  
/note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.5 kb. Library prepared by Life  
Technologies."

## ORIGIN

Query Match 2.3%; Score 86.4; DB 2; Length 503;

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Best Local Similarity 52.6%; Pred. No. 2.6e-06;
Matches 242; Conservative 0; Mismatches 206; Indels 12; Gaps 2;

QY 2088 CTTGGGTACAGGGGGCCGGGCTCTCGACCCACCTCCGGTTTACGTCGACCCCGT 2147
Db 21 CGAGACTACAGGGAGGCACTGTCTCGAGCCCTCAAGGGTACTACGACGTCCTCCCAT 80

QY 2148 GGTGGTGTGACCTTGGCAGGCTGTACCCAGCATCATCCAGGCCCAACCTGTGCTT 2207
Db 81 CGCCACCCTGGACTTCTCTCGCTGTACCCGTCATCATGTATGGCCCAACACCTGTGTTA 140

QY 2208 CAGTACGCTCTCCCTGCGGCCCGAGGCGGTCTCGGCACCTGAGGGCGGACCGGACTACCT 2267
Db 141 CACACAGCTCTCTCGGC-----CCGGACTGCACAGAAACTGGGCCCTGACTGAGGA 191

QY 2268 GGAGATCAGGTGGGGGCCGACGCGCTGTTCTTGTGAAGGCCCAACGCTACGCGAGAGCCT 2327
Db 192 TCAGTTTCATCAGGACCCCTCCCGGGGCGAGTTTGTGAAGACCTCAGTGGCGAAGGGGCT 251

QY 2328 GCTGAGCATCTGCTGCGGACTGGCTGGCCATCGGAAGCAGATCCGCTCGCGGATCCC 2387
Db 252 GCTGCCCCAGATCTCTGGAGAACCTGCTCAGTGCCTGGGAAGGGGCCAAGGCGGAGCTGGC 311

QY 2388 CCAGAGCAC---CCCGGAGGAGCGGCTCTCTCTGACAAAGCAACAGGCGCGCATCAAGGT 2444
Db 312 CAAGGAGACAGCCCTCCCGGCGCAGGTCTCTGATGAGCGGACGCTGGCGCTGAGGT 371

QY 2445 GGTGTGCAACTCGGTGTAAGGTTTACCGGGGCGCAGACCGTCTTTCGCCCTGCCGTGCA 2504
Db 372 GAGCGCCAACTCCGTATACGGCTTCACTGGGCGCCAGGTGGGCAAGTTGCGCGTGCCTGGA 431

QY 2505 CGTGCCGCCCACTGGAGACCATCGGCGCGAGATGCTC 2544
Db 432 GATCTCAGACGCGTCACGGGTTTCGGACGTCAGATGATC 471

RESULT 9
BX350425/c
LOCUS BX350425 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
DEFINITION CDNA clone CS0DK004YH13 3-PRIME, mRNA sequence.
ACCESSION BX350425
VERSION BX350425.2 GI:46550868
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 925)
AUTHORS Li W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 5, 2003 this sequence version replaced gi:30379510.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
9280.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?n=CS0BA1036ZG10_CS03439_1&c=9280.f

FEATURES
1. 925
Location/Qualifiers
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/clone="CS0DK004YH13"
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/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 2.3%; Score 85.4; DB 5; Length 925;
Best Local Similarity 50.9%; Pred. No. 4.1e-06;
Matches 259; Conservative 0; Mismatches 238; Indels 12; Gaps 2;

QY 2039 AGGACGGGGAGGAGCGAGGAGGTCCGCGCGAGAGCCGGGGCCGACGCTTCGCTACC 2098
Db 806 AGGCCATGCGACGAGGGGNTGCTGATGCCGCTCAAGGGTACTACGAGCTCCCATCGCCACCTGG 747

QY 2099 AGGGGGCCCGGGTCTCTCGACCCCACTCCCGGGTTTACGTCGACCCCGTGGTGTGTTG 2158
Db 746 CGGAAGCCACTGTCTATTGAGCCCTCAAGGGTACTACGAGCTCCCATCGCCACCTGG 687

QY 2159 ACTTTGCCAGCTGTATCCAGCATCATCAGGCCCAACACTGTGTTTACGTACGCTCT 2218
Db 686 ACTTCTCTCGCTGATCCCGTCCATCATGTATGGCCCAACCTGTGTTTACACCACTCC 627

QY 2219 CCCTGCGGCCGAGGCGGCTCGCGCACCTGGAGGGGAGCCGGGACTACTCTGGAGATCGAGG 2278
Db 626 TTCGGC-----CCGGACTGCACAGAAACTGGGCCCTGACTGAGGATCAGTTTCATCA 576

QY 2279 TGGGGGGCCGACGCGCTGTTCTTGTGAAGGCCCAACGCTACGCGAGAGCTGTCTGAGCATCC 2338
Db 575 GGACCCCCACCGGGGACGAGTTTGTGAAGACCTCAGTGCAGAGGGGCTGTGTCGCCCAGA 516

QY 2339 TGTGCGCGACTGTGTCGCATGCGAAAGCAGATCCCGCTCGCGGATCCCCCAGAGCAC-- 2396
Db 515 TCCTGGAGAACCTGCTCAGTGCCTGGAGAGGGGCAAGGCGGAGCTGCGCCAAAGAGACAG 456

QY 2397 -CCCCGAGGAGGCGGCTCTCTCTGACAAAGCAACAGGCGCGCATCAAGTGTGTGCAACT 2455
Db 455 ACCCTCTCGGCGCAGGTTCTGTGATGAGCGGCGAGCTGGCGCTGAAGGTGAGCGCCAACT 396

QY 2456 CGGTGTACGGGTTTACCGGGGCGCAGACCGTCTTCTGCTCCCTGCTGCACTGCGCCGCA 2515
Db 395 CCGTATACGGCTTCACTGGGCGCCAGGTGGGCAAGTTGCGGTGCTCGAGATCTCACAGA 336

QY 2516 CCGTACGACCATCGGCGCGAGATGCTC 2544
Db 335 CGGTACGCGGTTTCGGACGTCAGATGATC 307

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LOCUS BX053856
DEFINITION AGENCOURT 6874222 NIH_MGC_106 Homo sapiens cDNA clone IMAGE:5935767
5', mRNA sequence.
ACCESSION BX053856
VERSION BX053856.1 GI:19813196
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1368)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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http://image.llnl.gov  
Plate: LLCM2124 row: a column: 16  
High quality sequence stop: 219.

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Location/Qualifiers

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/note="Organ: blood; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 2.3%; Score 84.8; DB 5; Length 1368;  
Best Local Similarity 52.6%; Pred. No. 5.4e-06;  
Matches 239; Conservative 0; Mismatches 202; Indels 13; Gaps 2;

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QY 2096 ACCAGGGGCGGGTCTCGACCCACCTCCGGGTTTCACGTGACCCCGTGGTGT 2155
DB 1 ACACGGGAGCACTGTCTGACGCCCCCTCAAGGGTACTACAGCTCCCATCGCCACC 60
QY 2156 TTGACTTTGCCAGCTGTACCCAGCATCATCAGGCCACAACTGTCTTCAGTACGC 2215
DB 61 TGGACTTCTCTCTGTACCCGTCCATCATGATGCCCCACAACTGTGTACACACGC 120
QY 2216 TCTCCCTGGGCGGAGGCGCTCGGCACCTGGAGGGGACCGGACTACCTGGAGATCG 2275
DB 121 TCTTTCGGC-----CCGGGACTGCACAGAACTGGGCTGACTGAGGATCATGTTCA 171
QY 2276 AGGTGGGGGGCGAGCGCTGTTCTTCGTAAGGCCACAGTACGCGAGAGCCTGTGAGCA 2335
DB 172 TCATGACCCCAACCGGGAGAGTGTGTGAAGACTCAGTGGGAAGGGGTCTGTGCCCC 231
QY 2336 TCTGCTGGCGACTGTGGTGGCCATGCGAAAGCAGATCGCTTCGGGATGCCCCAG---- 2391
DB 232 AAATCTTGAGAACCTGTCTCAGTGGCCGGAAGAGGCCAAGCCGAGCTGGCCAAAGGAGA 291
QY 2392 AGCACCCCGGAGGCGCTCTCTCGACAGCAACAGCCGCGCATCAGGTGTGTGTC 2451
DB 292 CAGACCCCTCCGGCGCCAGGTCCTGGAATGGACCGGACGCTGGCGCTGAAAGGTGAGCGCC 351
QY 2452 AACTCGGTGTACGGTTACCGGGCGGAGCAGCGTCTTCTGCCCTGCTGACGCTGGCC 2511
DB 352 AACTCGGTATACGGTTTACTGGCGCCAGGTGGGCAAGTTGCCGTCTGAGATCTCC 411
QY 2512 GCCACCGTGAACCATCGGCGCGAGATGCTCC 2545
DB 412 CACAGCGTCACGGGTTCCGACGTCAGATGATCC 445
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## RESULT 11

B1118205  
LOCUS 602867491F1 NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:5015830 5',  
DEFINITION mRNA sequence.

ACCESSION B1118205

VERSION B1118205.1 GI:14569106

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 687)

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE  
JOURNAL  
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: LLCM1825 row: f column: 23  
High quality sequence stop: 674.  
Location/Qualifiers  
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/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

FEATURES  
source

Query Match 2.3%; Score 84.6; DB 4; Length 687;  
Best Local Similarity 51.1%; Pred. No. 5.8e-06;  
Matches 257; Conservative 0; Mismatches 234; Indels 12; Gaps 2;

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DB 134 AGGCCATGACGAGGGGCTGTGTGTCGGTGAAGTCAGAGGCGCGAGGACTACA 193
QY 2099 AGGGGGCGGGTCTCGACCCACCTCGGGTTTTCAGTTCGACCGCCGTTGGTGTG 2158
DB 194 CGGAGGCGACCTGTCTACGAGCCCTCAAGGGGTACTACGACGTCCTCCCATCGCCACCCCTGG 253
QY 2159 ACTTTGCGCAGCTGTACCCAGCATCTCAGGCCCAACCTGTGTCTTTCAGTACGCTCT 2218
DB 254 ACTTCTCTCGTGTACCCGTCCTCATCATGATGGGCCCAACCTGTGTACACACGCTCC 313
QY 2219 CCCTGCGGCCCGGAGCGCTCGCGCACCTGGAGGGCGGACCGGACTACCTGGAGATCGAGG 2278
DB 314 TTGGGC-----CCGGGACTGCACAGAACTGGGCTGACTGAGGATCAGTTTCATCA 364
QY 2279 TGGGGGGCGGAGCGCTGTTCCTGTGAAGGCCCACTGACGGGAGAGCCTGCTGAGCATCC 2338
DB 365 GGACCCCGCCCGGGAGCAGTGTGTGAAGACCTCAGTGCGAAGGGGTGCTGCCCCAGA 424
QY 2339 TGCTGGCGACTGTGCTGGCCATGCGAAGACAGATCCGCTCGCGGATCCCCAGAGACAC-- 2396
DB 425 TCCTGGAGAACCTGCTCAGTGGCCGGAAGAGGCCCAAGCCGAGCTGGCCAAAGGAGACAG 484
QY 2397 -CCCCGAGGAGCGCTCTCTCTCGACAAAGCCGCGCCCATCAAGGTGGTGTGCAACT 2455
DB 485 ACCCCCTCGGGCGCCAGGTCTCTGGATGGACGGCAGCTGCGCGTGAAGGTGAGCGCAACT 544
QY 2456 CGGTGTACGGGTTACCGGGGCGGACGACGGTCTTCTGCGCTGCTGCTGACGCTGGCGGCA 2515
DB 545 CCGTATACGGTTTCACTGCGGCCCGGAGTGGGCAAGTTGCCGTGCTGAGATCTCACAGA 604
QY 2516 CCGTGACCAACCATCGGCGCGAG 2538
DB 605 GCGTACCGGGGTTCGAGCGTCAG 627
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## ORIGIN

Query Match 2.3%; Score 84.6; DB 4; Length 687;  
Best Local Similarity 51.1%; Pred. No. 5.8e-06;  
Matches 257; Conservative 0; Mismatches 234; Indels 12; Gaps 2;

```
QY 2039 AGGACGGGAGCGAGCGGAGGAGTTCGGCGCGAGACCGGGCGCGGACGTTGGGTACC 2098
DB 134 AGGCCATGACGAGGGGCTGTGTGTCGGTGAAGTCAGAGGCGCGAGGACTACA 193
QY 2099 AGGGGGCGGGTCTCGACCCACCTCGGGTTTTCAGTTCGACCGCCGTTGGTGTG 2158
DB 194 CGGAGGCGACCTGTCTACGAGCCCTCAAGGGGTACTACGACGTCCTCCCATCGCCACCCCTGG 253
QY 2159 ACTTTGCGCAGCTGTACCCAGCATCTCAGGCCCAACCTGTGTCTTTCAGTACGCTCT 2218
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RESULT 12	AJ723868	727 bp	mRNA	linear	EST 07-OCT-2004
LOCUS	AJ723868	rikem1 Gallus gallus cDNA clone 26j22e5,	mRNA sequence.		
DEFINITION	AJ723868	rikem1 Gallus gallus cDNA clone 26j22e5,	mRNA sequence.		
ACCESSION	AJ723868	rikem1 Gallus gallus cDNA clone 26j22e5,	mRNA sequence.		
VERSION	AJ723868.1	GI:53889282			
KEYWORDS	EST.				
SOURCE	Gallus gallus (chicken)				
ORGANISM	Gallus gallus				
REFERENCE	1	(bases 1 to 727)			
AUTHORS	Caldwell,R.B., Kierzek,A.M., Arakawa,H., Bezzubov,Y., Zaim,J., Friedler,P., Kutter,S., Blagodatski,A., Kostovska,D., Koter,M., Archosouria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.				
TITLE	Full-length cDNAs from bursal lymphocytes to facilitate gene function analysis				
JOURNAL	Unpublished (2004)				
COMMENT	Contact: Caldwell RB				
FEATURES	Source	Location/Qualifiers			
ORIGIN	Query Match	2.3%; Score 84.2; DB 1; Length 727;			
	Best Local Similarity	47.2%; Pred. No. 6.9e-06;			
	Matches 297; Conservative	0; Mismatches 323; Indels 9; Gaps 1;			
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DB	660	GGAGTTTGTGCGCAATTTGTGACCGCGGAGTCAATCAACGCGGTACAACTCCAGAACTTCGA	601		
QY	1416	CTGCGCTTCTGCTGCTGACCAAGCTGACGAGATCTACAAAGTCCCGCTCGACGGGTACGG	1475		
DB	600	CTGCGCTTCTGCTGCTGACCGCGCGAGTGTCTAGGGTCTGCTTCCCGTCTCTGGG	541		
QY	1476	GCGCATGAACCGCGCGGCGTGTCTCGCGTGTGGACATCGCGCCAGAGCCACTTTCAGAA	1535		
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DB	420	GCTGCTCGGGAGCAAACTCGGCTCTTATACCTCTAATGGGTTCAGCGGCGATTTCTCT	361		
QY	1647	GAGAGCAAGAGAGGATCTGAGCTGACGCGAGATATTCGTGAGGACTTCGCTGCTCGGGCC	1706		
DB	360	GCACGAGCAGAGAGGAGAGTATCCCATAGCATCATACCGACCTTACAGCACGGCTCGGA	301		
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DB	300	TCAGACGCGCGCGCTGCGCTGTATCTGCTGAGGACGAGTGTCTGCGCTCTGCGCT	241		
QY	1767	GTTCCTTCAAGTTCTGCCGCACTGGAGCTTTCCGCGCTCGCGCGCTTGGCGGCGATCAA	1826		
DB	240	GTTCGAGCGGCTGATGCTGTGTGTGAACCACTGAGGATGGCGCGCTCAACCGGCTCCC	181		

QY	1827	CATCACCGCACCATCTACAGCGCGCAGACATCCGCGTCTTACGTCGCTCTCTGGCGCT	1888		
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QY	1887	TGCGGGCCAGAGGGCTTCATCTCTGCGGG	1915		
DB	120	GGCCATGCAGGAGGATCTGCTGCGCGG	92		
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LOCUS	CG754548/c	P050-1-All.za Ppa EcoRI BAC library Pristionchus pacificus genomic,	genomic survey sequence.		
DEFINITION	CG754548	P050-1-All.za Ppa EcoRI BAC library Pristionchus pacificus genomic,	genomic survey sequence.		
ACCESSION	CG754548	P050-1-All.za Ppa EcoRI BAC library Pristionchus pacificus genomic,	genomic survey sequence.		
VERSION	CG754548.1	GI:37980151			
KEYWORDS	GSS.				
SOURCE	Pristionchus pacificus				
ORGANISM	Pristionchus pacificus				
REFERENCE	1	(bases 1 to 1956)			
AUTHORS	Srinivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K., Buntjer,J., van der Meulen,M. and Sommer,R.J.				
TITLE	An integrated physical and genetic map of the nematode Pristionchus pacificus				
JOURNAL	Mol. Genet. Genomics 269 (5), 715-722 (2003)				
MEDLINE	22835951				
PUBMED	12884007				
COMMENT	Contact: Sommer RJ				
	Evolutionary Biology				
	Max-Planck-Institute for Developmental Biology				
	Spemannstr. 37-39, Tuebingen D-72076, Germany				
	Tel: 00497071601371				
	Fax: 00497071601498				
	Email: ralf.sommer@tuebingen.mpg.de				
	Class: BAC ends.				
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source	1. 1956				
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	/note="The library was generated by a partial digest of the genomic DNA with EcoRI and cloning into the BAC vector."				
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	Best Local Similarity	33.7%; Pred. No. 1.7e-05;			
	Matches 543; Conservative	0; Mismatches 1053; Indels 15; Gaps 3;			
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DB	1713	CCCGCGCCCG	1654		
QY	1892	GCCAGAGGGCTTCATCTGCGCGACACCCAGGGCGGCTTTCGGGGGCTTCGACAAAGGAGG	1951		
DB	1653	CCCG	1594		
QY	1952	CGCCACAGCGCCCGCGCTGCTCGGGGGGAAGGGGAGCGGCGCGGGGGAGCGGAGACGGGG	2011		
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QY 2252 CGGACCGGACTTACCTGGAGATCGAGGTGGGGCGCGAGCGTGTCTTCTGTGAAGGCC 2311
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RESULT 14
BP096735 453 bp mRNA linear EST 30-JUN-2004
LOCUS
DEFINITION BP096735 Chlamydomonas reinhardtii C9 various conditions
Chlamydomonas reinhardtii cDNA clone MXL063h11_r 5', mRNA sequence.
ACCESSION BP096735
VERSION BP096735.1 GI:49468874
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadales; Chlamydomonas.
REFERENCE 1 (bases 1 to 453)
AUTHORS Asamizu,E., Nakamura,Y., Miura,K., Fukuzawa,H., Fujiwara,S.,
Hirono,M., Iwamoto,K., Matsuura,Y., Minagawa,J., Shimogawara,K.,
Takahashi,Y. and Tabata,S.
TITLE Establishment of Publicly Available cDNA Material and Information
Resource of Chlamydomonas reinhardtii (Chlorophyta), to Facilitate
Gene Function Analysis
JOURNAL Phycologia (2004) In press
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES
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XhoI; The cDNA library was made from a mixture of cells
grown under various conditions"

ORIGIN
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Best Local Similarity 51.9%; Pred. No. 1.8e-05;
Matches 218; Conservative 0; Mismatches 190; Indels 12; Gaps 1;

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Db 121 TGGTTCTGTGCGAACAGCGCGGCAACGCGGCGCTGTGTGCGAGAGATTTCTGAGAGAGCTGTG 180
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## RESULT 15

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LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC
DEFINITION BACN03P19 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
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ACCESSION

VERSION AL098882.1 GI:5610493

KEYWORDS

SOURCE GSS.

ORGANISM Drosophila melanogaster (fruit fly)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1009)

Genoscope.

Direct Submission

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a  
collaboration with the European Drosophila Genome Project (EDGP) -  
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC  
library (Dros BAC) was made by Alain Billaud at CEPH (Centre  
d'Etude du Polymorphisme Humain) with funding provided by a MRC  
project grant. The DNA was prepared from embryos by Alain Bucheton  
and Genevieve Payan. It has been constructed in the vector  
pBelOBAC11.

## FEATURES

source

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Best Local Similarity 29.7%; Pred. No. 2.2e-05;
Matches 131; Conservative 112; Mismatches 198; Indels 0; Gaps 0;

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Qy 2041 GACGGGAGCGAGCGGAGGAGTTCGCGCGCAGAGCAGGGGGCGGCGACGTTGGGTAC 2100  
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Qy 2101 GGGGCGCGGTTCTGACCCCACTTCGGGTTTTCAGCTCGACCCCGCTGCTGCTGTTGAC 2160  
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Qy 2161 TTTGCGAGCTTACCCAGCATCATCAGGCGGCAACCTGCTTTCAGTACGCTCTCC 2220  
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QY 2281 GGGGGCCGACGGCTGTCTTCTGTGAAGGCCACAGTACGCGAGAGCTGTCTGAGCATCTGT 2340
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## RESULT 2

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US-10-692-556-1
; Sequence 1, Application US/10692556
; Publication No. US20040115623A1
; GENERAL INFORMATION:
; APPLICANT: Homa, Fred
; APPLICANT: Wathen, Michael
; APPLICANT: Hopkins, Todd
; APPLICANT: Thomsen, Darrell
; TITLE OF INVENTION: A Method for Treating Herpes Virus
; FILE REFERENCE: 00221
; CURRENT APPLICATION NUMBER: US/10/692,556
; CURRENT FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3717
; TYPE: DNA
; ORGANISM: herpes simplex
US-10-692-556-1
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Query Match 100.0%; Score 3717; DB 19; Length 3717;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB |||||
DB 121 CGCGGAGAGACTTCTACAAACCCCTCGCTCAGACGGGAGCCAGCCAAAGGCCCC 180
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DB 181 GGGCGGCTCAGCGCCATACCTACTACAGCAGTGCAGCAATTTTCGATTTATCCGCCG 240
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RESULT 3  
US-09-904-065-3  
; Sequence 3, Application US/09904065  
; Patent No. US20020076789A1  
; GENERAL INFORMATION:  
; APPLICANT: Homa, Fred  
; APPLICANT: Wathen, Michael  
; APPLICANT: Hopkins, Todd  
; APPLICANT: Thomsen, Darrell  
; TITLE OF INVENTION: A Method for Treating Herpes Virus  
; FILE REFERENCE: 00221  
; CURRENT APPLICATION NUMBER: US/09/904,065  
; CURRENT FILING DATE: 2001-07-12  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 3723  
; TYPE: DNA  
; ORGANISM: herpes simplex  
US-09-904-065-3  
Query Match 99.4%; Score 3696.2; DB 9; Length 3723;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 3714; Conservative 0; Mismatches 3; Indels 6; Gaps 1;  
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## RESULT 4

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US-10-692-556-3
; Sequence 3, Application US/10692556
; Publication NO. US20040115623A1
; GENERAL INFORMATION:
; APPLICANT: Homa, Fred
; APPLICANT: Wathen, Michael
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; APPLICANT: Hopkins, Todd
; APPLICANT: Thomsen, Darrell
; TITLE OF INVENTION: A Method for Treating Herpes Virus
; FILE REFERENCE: 00221
; CURRENT APPLICATION NUMBER: US/10/692,556
; CURRENT FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 3723
; TYPE: DNA
; ORGANISM: herpes simplex
US-10-692-556-3
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Query Match 99.4%; Score 3696.2; DB 19; Length 3723;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 3714; Conservative 0; Mismatches 3; Indels 6; Gaps 1;

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US-09-827-688-8  
; Sequence 8, Application US/09827688  
; Publication No. US20030165476A1  
; GENERAL INFORMATION:  
; APPLICANT: KINSEY, FRANK  
; APPLICANT: KINSEY, BERMA  
; APPLICANT: BHOGAL, BALBIR  
; TITLE OF INVENTION: MACROAGGREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION  
; TITLE OF INVENTION: AGENTS  
; FILE REFERENCE: P01949US1/10004014  
; CURRENT APPLICATION NUMBER: US/09/827,688  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/195,680  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 154746  
; TYPE: DNA  
; ORGANISM: HERPESVIRUS 2

US-09-827-688-8  
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Best Local Similarity 99.7%; Pred. No. 0;  
Matches 3712; Conservative 0; Mismatches 5; Indels 6; Gaps 1;  
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Qy 61 TCTGGGTTTTTGGCCCCCAACACCCCGGGGAGCACCCAGACGCGACCGCGCTTGC 120  
Db 63325 TCTGGGTTTTTGGCCCCCAACACCCCGGGGAGCACCCAGACGCGACCGCGCTTGC 63384  
Qy 121 CGCGGAGAACTTCTACAACCCCACTCGCTCAGACCGGAAACGAGCAAGAGCCGCC 180  
Db 63385 CGCGGAGAACTTCTACAACCCCACTCGCTCAGACCGGAAACGAGCAAGAGCCGCC 63444  
Qy 181 GGGCGGCTCAGCGCATACGTACTACAGCGAGTGCAGAAATTTTCGATTTATCGCCCG 240  
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Qy 361 GAGGCTTCTGCGCGCTCGCTTGGCGCTGTGGGGCGGTGGCGGACCATGCCCCCAAGGG 420  
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QY	1021	GACGTCGAGTTTAACTGCA CGGCGGA CAACCTGGCCGTCGAGGGGGCCATGTGTGACCTG	1080	QY	2095	TACAGGGGGCCCGGGTCCTCGACCCCACTCCGGGTTTCA CGTCGACCCCGTGGTGGTG	2154
Db	64285	GACGTCGAGTTTAACTGCA CGGCGGA CAACCTGGCCGTCGAGGGGGCCATGTGTGACCTG	64344	Db	65365	TACAGGGGGCCCGGGTCCTCGACCCCACTCCGGGTTTCA CGTCGACCCCGTGGTGGTG	65424
QY	1081	CGGGCTTACAAGCTCATGTGCTTCGATATCGAATCGAAGGCGGGGGGAGGACGAGCTG	1140	QY	2155	TTTGACCTTTGCGACGCTGTACCCAGCATCATCAGAGCCCAACAACCTGTCTCAGTACG	2214
Db	64345	CGGGCTTACAAGCTCATGTGCTTCGATATCGAATCGAAGGCGGGGGGAGGACGAGCTG	64404	Db	65425	TTTGACCTTTGCGACGCTGTACCCAGCATCATCAGAGCCCAACAACCTGTCTCAGTACG	65484
QY	1141	GCCTTTCGGGTGCGGGAAGCGCCGGAAGACCTCGTCATCCAGATCTCCTGTCTGTCTTAC	1200	QY	2215	CTCTCCCTGCGGCGCGAGGCGCTCGCGACCTGAGGGCGGACCGGGACTACTCTGGAGATC	2274
Db	64405	GCCTTTCGGGTGCGGGAAGCGCCGGAAGACCTCGTCATCCAGATCTCCTGTCTGTCTTAC	64464	Db	65485	CTCTCCCTGCGGCGCGAGGCGCTCGCGACCTGAGGGCGGACCGGGACTACTCTGGAGATC	65544
QY	1201	GACCTGTCCACGACCGCCTCGAGACATATCTCTCTGTGTTTTCGTCGGAATCCTGGACCTC	1260	QY	2275	GAGTGGGGGGCCGACCGGCTGTTCTTCTGTAAGGCCACAGTACGGGAGAGGCTGCTGAGC	2334
Db	64465	GACCTGTCCACGACCGCCTCGAGACATATCTCTCTGTGTTTTCGTCGGAATCCTGGACCTC	64524	Db	65545	GAGTGGGGGGCCGACCGGCTGTTCTTCTGTAAGGCCCACTGACGTAACGAGGCTGCTGAGC	65604
QY	1261	CCCGAGTCCCACTCAGCGATCTGCGCTCCAGGGSCCTGCGGCCCGCCGTCGTCCTGGAG	1320	QY	2335	ATCTCTGTGCGGACTCGCTGGCCCATCGAAAGCAGATCGCTCGCGATCCCCCAGAGC	2394
Db	64525	CCCGAGTCCCACTCAGCGATCTGCGCTCCAGGGSCCTGCGGCCCGCCGTCGTCCTGGAG	64584	Db	65605	ATCTCTGTGCGGACTCGCTGGCCCATCGAAAGCAGATCGCTCGCGATCCCCCAGAGC	65664
QY	1321	TTTGACGCGAATTCGAGATGCTGCTGCTTCATGACCTTCGTCAAGCAGTACGGGCC	1380	QY	2395	ACCCCGAGGAGGCGCTCTCTCGACAAGCAACAGGCGCGCATCAAGGTGGTGTGCAAC	2454
Db	64585	TTTGACGCGAATTCGAGATGCTGCTGCTTCATGACCTTCGTCAAGCAGTACGGGCC	64644	Db	65665	ACCCCGAGGAGGCGCTCTCTCGACAAGCAACAGGCGCGCATCAAGGTGGTGTGCAAC	65724
QY	1381	GAGTTCGTGACGGGTACAACATCATCAATCTTCAAGCTGCGCTTCGTCTGACCAAGCTG	1440	QY	2455	TCGCTGTACGGGTTCA CGGGGCGCAGCA CGGTCTTCTGCGGCTGCTGCGAGTGGCGGCC	2514
Db	64645	GAGTTCGTGACGGGTACAACATCATCAATCTTCAAGCTGCGCTTCGTCTGACCAAGCTG	64704	Db	65725	TCGCTGTACGGGTTCA CGGGGCGCAGCA CGGTCTTCTGCGGCTGCTGCGAGTGGCGGCC	65784
QY	1441	ACGAGATCTACAAGTCCCGCTCGACGGGTACGGGCGCATGACGGCGGGGTGTGTTTC	1500	QY	2515	ACCGTGAAGCAATCGCGCGAGATGCTCTCGCGACGCGCGGTACGTGCA CGCGGCC	2574
Db	64705	ACGAGATCTACAAGTCCCGCTCGACGGGTACGGGCGCATGACGGCGGGGTGTGTTTC	64764	Db	65785	ACCGTGAAGCAATCGCGCGAGATGCTCTCGCGACGCGCGGTACGTGCA CGCGGCC	65844
QY	1501	CGCGTGTGGGACATCGGCGAGAGCCATTTTCAGAGCGCAGCAAGATCAAGGTGAACGGG	1560	QY	2575	TGGCGGAGTTTCGATCAGCTGCTGCGCGACCTTTCGAGGCGCGCGCATGCGCGGCC	2634
Db	64765	CGCGTGTGGGACATCGGCGAGAGCCATTTTCAGAGCGCAGCAAGATCAAGGTGAACGGG	64824	Db	65845	TGGCGGAGTTTCGATCAGCTGCTGCGCGACCTTTCGAGGCGCGCGCATGCGCGGCC	65904
QY	1561	ATGTTGAACATCGACATGTAGCGCATCATACCGACAAGGTCAAATCTCAGCTACAAAG	1620	QY	2635	GGTCCGTACTCCATGCGCATCATCTACGGGACAGGACTCCATTTTCGTTTGTGGCGC	2694
Db	64825	ATGTTGAACATCGACATGTAGCGCATCATACCGACAAGGTCAAATCTCAGCTACAAAG	64884	Db	65905	GGTCCGTACTCCATGCGCATCATCTACGGGACAGGACTCCATTTTCGTTTGTGGCGC	65964
QY	1621	CTGAACCGCCTCGCGAGCGCTCTTGAAGACAGAGAGGATCTGAGCTACCGGAC	1680	QY	2695	GGCTCTACGGCGCGCGCTGTTGGCCATGAGGCGCAAGATGAGGAGCCACATCTCGGCC	2754
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QY	1681	ATCCCGCCTTACTAGCCTTCGCGGCCCGCGCAGCGCGGGGTGATCGGCGAGTATTGTGTG	1740	QY	2755	GCGCTGTTCCTCCCGCATCAAGCTCGAGTGGGAAAGAAAGGTTTCA CCAAGCTGCTGCTC	2814
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QY	1741	CAGGACTCGCTGCTGGGAGCTGTCTTCAAGTTTCTGCGGACCTGGAGCTTTCC	1800	QY	2815	ATCGCAAGAAAAGTACATCGGCGTCACTGCGGGGCGAGATGCTCATCAAGGGCGGTG	2874
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QY	1801	GCGGTCGCGCGCTGGGGGATCAACATCACCGCACCATCTACGAGCGGCGCAGAGATC	1860	QY	2875	GATCTGTGGCGCAAAAAAACA CTGCGCTTTATCAACCGCACCTCCAGGGCCCTTGGTGCAC	2934
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Db	65125	CGCGTCTTCA CGTGCTCTCGCTTCGCGGCCAGAAAGGCTTCATCTCTCCCGGACACC	65184	Db	66205	CTGCTGTTTTCAGCAGATACCGTATCCGAGCGCGCCCGCGGTTAGCGAGGCGCCCGCA	66264
QY	1921	CAGGGCGGTTTCGGGGCTTCGACGAGGCGGCCCAAGCGCCCGCGCTGCTCGGGG	1980	QY	2995	GAGGAGTGGCTGGCGGACCCCTGCGCGAGGACTGCGAGGTTTCGGGGCGCTCCTCGTA	3054
Db	65185	CAGGGCGGTTTCGGGGCTTCGACGAGGCGGCCCAAGCGCCCGCGCTGCTCGGGG	65244	Db	66265	GAGGAGTGGCTGGCGGACCCCTGCGCGAGGACTGCGAGGTTTCGGGGCGCTCCTCGTA	66324
QY	1981	GAAAGGGAGCGGCGGGGACCGGAAACCGGACAGAGATTAAGGACGACGACGA ----G	2034	QY	3055	GACGCCCATCGGCGCATCA CCGACCCGAGAGGAGCATTCAGGACTTTGTCTTCA CCGGCC	3114
Db	65245	GAAAGGGAGCGGCGGGGACCGGHAACGGGACGAGGATTAAGGACGACGACGAGCGGG	65304	Db	66325	GACGCCCATCGGCGCATCA CCGACCCGAGAGGAGCATTCAGGACTTTGTCTTCA CCGGCC	66384
QY	2035	GAAGGAGCGGGGACGAGCGGAGGAGGTTCGCGCGAGACCGGGGGCCGCA CTTTGGG	2094	QY	3115	GAACTGAGCAGACACCCGCGCGGTACA CCAACAGCGCTTGGCCCACTGACGGTGTAT	3174
Db	65305	GACGAGGACGGGACGAGCGGAGGAGGTTCGCGCGAGACCGGGGGCCGCA CTTTGGG	65364	Db	66385	GAACTGAGCAGACACCCGCGCGGTACA CCAACAGCGCTTGGCCCACTGACGGTGTAT	66444
				QY	3175	TACAAGCTCATGGGCCCGCGCGCAGGTCCCGTCCATCAAGGACCGGATCCCGTACGCTG	3234

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Qy 3715 TGA 3717
Db 66985 TGA 66987
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US-09-904-065-5  
; Sequence 5, Application US/09904065  
; Patent No. US20020076789A1  
; GENERAL INFORMATION:  
; APPLICANT: Homa, Fred  
; APPLICANT: Mathen, Michael  
; APPLICANT: Hopkins, Todd  
; APPLICANT: Thomsen, Darrell  
; TITLE OF INVENTION: A Method for Treating Herpes Virus  
; FILE REFERENCE: 00221  
; CURRENT APPLICATION NUMBER: US/09/904,065  
; CURRENT FILING DATE: 2001-07-12  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 3708  
; TYPE: DNA  
; ORGANISM: herpes simplex  
US-09-904-065-5

Query Match 82.3%; Score 3059.8; DB 9; Length 3708;  
Best Local Similarity 89.3%; Pred. No. 0;  
Matches 3321; Conservative 0; Mismatch 387; Indels 9; Gaps 2;

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Qy 1 ATGTTTTGTGCGCGCGCGCGCGCTTCCCGCGGGGAGTTCGGCGGCTCGCGCGCGG 60
Db 1 ATGTTTTGTGCGCGCGCGCGCGCTTCCCGCGGGGAGTTCGGCGGCGCGCGCGG 60
Qy 61 TCTGGGTTTTTGGCCCCCACAACCCCGGGGAGCCACCGAGCGGACCGCGCGCTTGC 120
Db 61 TCCGGGTTTTTGGCGCGCGCGCGCGCTTCCCGGAGCGCGC---GGGGACCCCGCGCTTGT 117
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1198	Db	 GACGTGTCACACCGCGCTGGAGCAGTCTCTCTGTTTTCGTTCGGTTCCTGCGACCTC	1257
1261	Qy	 CCCGAGTCCCAACCTCAGCGATCTCGCTCCAGAGGGGCTCGCGGCCCGCGTCTGTCGGAG	1320
1258	Db	 CCCGAAATCCCACTGAAACGAGCTGGCGGCCAGGGGCTGCGCACGCCCGGTGTTCTGGA	1317
1321	Qy	 TTTGACAGCGAATTCGAGATGCTGCTGGCCCTTCATGACCTTCGTCAAGCAGTACGGCCCC	1380
1318	Db	 TTCGACAGCGAATTCGAGATGCTGTTGGCTTCATGACCTTGTGAACAGTACGGCCCC	1377
1381	Qy	 GAGTTCTGTACCCGGGTAAACAATCATCAACTTCGACTGGCCCTTCGTCTGACCAAGCTG	1440
1378	Db	 GAGTTCTGTACCCGGGTAAACAATCATCAACTTCGACTGGCCCTTCGTCTGCGCAAGTTG	1437
1441	Qy	 ACGAGATCTACAGGTCCTCGCTCGACGGGTACGGGGCGATGAACGGCCGGGTGTGTTTC	1500
1438	Db	 ACGGACATTTACAAGTCTCCCTCGACGGGTACGGCCGCATGAACGGCCGGGCGGTGTTT	1497
1501	Qy	 CGCGTGTGGACATCGCGCAGAGCCATTTTCAGAAAGCGCAGCAAGATCAAGGTGAACGGG	1560
1498	Db	 CGCGTGTGGACATAGCGCAGAGCCATTTTCAGAAAGCGCAGCAAGATCAAGGTGAACGGC	1557
1561	Qy	 ATGGTGAACATCGACATGTATCGGCATCATCACCGACAAGGTCAAACCTCTCCAGCTACAAG	1620
1558	Db	 ATGGTGAACATCGACATGTATCGGCATCATTAACCGACAAGATCAAGCTCTCGAGCTACAAG	1617
1621	Qy	 CTGAACCGCTCGCGAGGGCGTCTTGAAGGACNAGAAAGAGATCTGAGCTACCGGGAC	1680
1618	Db	 CTCAACCCCGTGGCCGAAGCCGCTCTGAAGGACNAGAAAGAGACTGAGCTATCCGCAC	1677
1681	Qy	 ATCCCCGCTACTACGCTCTCGGCGCGCGCAGCGCGGGTGTATCGSCGAGTATTGTGTC	1740
1678	Db	 ATCCCCGCTACTACGCGCGCGGCGCCGCGAACGCGGGGTGATCGCGGAGTACTGCATTA	1737
1741	Qy	 CAGGAATCGCTGTGGTCTGGGCGAGCTGTTCTTCAAGTTTCTGCGCGCACCTGTGAGCTTTC	1800
1738	Db	 CAGGAATCCCTGTGTTGGCGAGCTGTGTTTTTAAGTTTGTGCCCATCTGGAGCTCTCG	1797
1801	Qy	 GCCGTTCGCGCGCTGGCGGGGATCAACATCACCGGCACATCTACNAGCGCGCAGCAGATC	1860
1798	Db	 GCCGTTCGCGCGCTGGCGGGGTATTAACATCACCGGCACCACTACNAGCGCGCAGCAGATC	1857
1861	Qy	 CGCGTCTTACGTGCTCTCGCGCTTGGCGGCCAGAAAGGGCTTCATCTGCGCGGACACC	1920
1858	Db	 CGCGTCTTACGTGCTCTCGCGCTGCGCTGCGGACCAAGAAAGGCTTATCTTCCCGGACACC	1917
1921	Qy	 CAGGGCGGTTTCGGGCGCTCGACAAGGAGCGGCCAAGCGCCCGGCGCTGCTCGGGGG	1980
1918	Db	 CAGGGCGGATTTAGGGCGCGCGGGGGAGGGCGGCCCAAGCGTCGCGCGCAGCCCCGGGAG	1977
1981	Qy	 GAAGGGAGCGCGCGGGGACCGGGAACGGGGAACGAGGATTAAGACGACGACGAGGACGAG	2040
1978	Db	 GACGAGAGCGGCGCAGGAGGAGGGGGGAGGAGACG-----AGGACGAAACGCGAGGAGGGC	2031
2041	Qy	 GACGGGACAGCGCGAGGAGGTTCGCGCGGAGACCGGGGCGCGGACGTTGGGTACCGAG	2100
2032	Db	 GGGGCGAGCGGGAGCCCGGAGGGCGCGGGGAGACCGCCGCGCGGACGTTGGGGTACCGAG	2091
2101	Qy	 GGGGCCCGGGTCTTCGACCCCAACCTCCGGGTTCACGTCGACCCCGTGGTGGTGTTCGAC	2160
2092	Db	 GGGGCCAGGGTCTTTCGACCCCACTTCCTGGGTTCACGTCGAACCCCGTGGTGGTGTTCGAC	2151
2161	Qy	 TTTGCGACCTGTATCCCGAGCATCATCAGGCCCAACAACTGTGCTTCAGTACGCTCTCC	2220
2152	Db	 TTTGCGACCTGTATCCCGAGCATCATCAGGCCCAACAACTGTGCTTCAGCAGCGCTCTCC	2211
2221	Qy	 CTCGGGCCCGAGGGCGTTCGCGCACCTTCGAGCGCGGACCGGGACTACCTGGAGATCGAGGTG	2280
2212	Db	 CTGAGGGCCGACGACGTGGCGCACCTTCGAGCGGGGCAAGGACTACCTTGGAGATCGAGGTG	2271
2281	Qy	 GGGGGCCGACGGCTGTTCTTCGTGAAGGCCCAACGTCACGCGAGAGCCGTGTGAGCATCTCTG	2340

Db	2272	GGGGGGCGACGGCTGTTCTTCTGTCAAAGGCTCACGTGCGAGAGAGCCCTCTCTCAGCATCCTC	2333
Qy	2341	CTGCGGCACTGGCTGGCCATGCGAAAGCAGATCCGCTCGCGGATCCCCAGAGCACCCCCC	2400
Db	2332	CTGCGGACCTGGCTCGCCATGCGAAGCAGATCCGCTCGCGGATTTCCCNAGACGAGCCCC	2391
Qy	2401	GAGGAGCCCGTCTCTCTCGACAAGCAACAGGCGGCCCATCAAGGTGGTGTGCAACTCGGTG	2460
Db	2392	GAGGAGSCCGTGCTCTCTGGACAAGCAGCAGGCGCCCATCAAGGTGCTGTGTAACTCGGTG	2451
Qy	2461	TACGGGTTCAACGGGGCGCAGACGGTCTTCTGCTCTGCTGCTGCACTGCGTGGCCGCCACCGTG	2520
Db	2452	TACGGGTTCAACGGGAGCGCAGCAGGACTCTCTGCGCTGCTGCACTGCTGCGCGACGCGTG	2511
Qy	2521	ACGACCATCGGCGCGAGATGCTCTTCGGACGCGCGCGTACGTGCAACGCGCGCTCGGGG	2580
Db	2512	ACGACCATCGGCGCGAGATGCTGCTGCGACCCGCGAGTACGTCCACGCGCGCTCGGGG	2571
Qy	2581	GAGTTTCATCAGCTGCTGGCGGACTTTTCGGAGGCGCGCGCATGCGCGCCCCCGGTCGG	2640
Db	2572	GCCTTCGAACAGCTCTCTGGCCGATTTCCCGGAGGCGCGCGCATGCGCGCCCCCGGCCCC	2631
Qy	2641	TACTCCATGCGCATCATCTACGGGGAACGGGAACATCTATTTTGGTTTTGTCGCGGCGCTC	2700
Db	2632	TATTTCCATGGCATCATCTACGGGGAACGGACTTCCATATTTGTGTGTGTCGCGGCGCTC	2691
Qy	2701	ACGCGCGGGGCTGGTGGCCATGGGCGACAGATGGCGAGCCACATCTCGCGCGCGCTG	2760
Db	2692	ACGCGCGGGGCTGACGGGCCATGGGCGACAGATGGCGAGCCACATCTCGCGCGCGCTG	2751
Qy	2761	TTCTCTCCCCCGGATCAAGCTCGAGTGCAGAAAAAGCTTACCAAGCTGCTGCTCATCGCC	2820
Db	2752	TTTCTGCCCCCATCAAACTCGAGTGGAAAAAGCGTTCAACCAAGCTGCTGCTGATCGCC	2811
Qy	2821	AAGAAAAAGTACATCGCGCTCATCTCGGGGGCAAGATGCTCATCAAGGCGCTGGATCTG	2880
Db	2812	AAGAAAAAGTACATCGCGCTCATCTCGGGGGTAAAGATGCTCATCAAGGCGCTGGATCTG	2871
Qy	2881	GTGCGCAAAACAACTCGCGTTTATCAACCGCACCTTCAGAGGCGCTGCTGCACTGCTG	2940
Db	2872	GTGCGCAAAACAACTCGCGGTTTATCAACCGCACCTTCAGAGGCGCTGCTGCACTGCTG	2931
Qy	2941	TTTTTACGAGTACCGGTATCCGAGGCGCGCGCGCTTAGCCGAGCGCCCGCAGAGGAG	3000
Db	2932	TTTTTACGAGTACCGGTATCCGAGGCGCGCGCGCTTAGCCGAGCGCCCGCAGAGGAG	2991
Qy	3001	TGGCTGCGCGACCCCTGCCCGAGGAGCTGCAAGCGTTTCGGGGCGCTCTCTGTTAGACGCC	3060
Db	2992	TGGCTGCGCGACCCCTGCCCGAGGAGCTGCAAGCGTTTCGGGGCGCTCTCTGTTAGACGCC	3051
Qy	3061	CATCGCGGATCACCGNACCGGAGAGGGAACATCCAGGACTTTGTGCTCTCACCGCGCACTG	3120
Db	3052	CATCGCGGATCACCGNACCGGAGAGGGAACATCCAGGACTTTGTGCTCTCACCGCGCACTG	3111
Qy	3121	AGCAGACACCGCGCGGTACACAAACAGCGCTTCGCCACCTGACGGTGTATTACAAG	3180
Db	3112	AGCAGACACCGCGCGGTACACAAACAGCGCTTCGCCACCTGACGGTGTATTACAAG	3171
Qy	3181	CTCATGCCCCCGCGCGCAGGTCCCGTCCATCAAGGACCGGATCCCGTACGTGATCGTG	3240
Db	3172	CTCATGCCCCCGCGCGCAGGTCCCGTCCATCAAGGACCGGATCCCGTACGTGATCGTG	3231
Qy	3241	GCCCAGACCCGCGAGGTAGAGGAGACGGTTCGCGGGCTGGCGGCTTCGCGAGCTAGAC	3300
Db	3232	GCCCAGACCCGCGAGGTAGAGGAGACGGTTCGCGGGCTGGCGGCTTCGCGAGCTAGAC	3291
Qy	3301	GCGCGCCGCCACAGGGAGCAGCCCGCCCCCGCCACAGCGGCGCTGCGCTTCCCGCCAGCGC	3360
Db	3292	GCGCGCCGCCACAGGGAGCAGCCCGCCCCCGCCCGCGGCGCTGCGCTTCCCGCCAGCGC	3351
Qy	3361	CCCCGGGAGACGCGCTGCGATGCGGACCCCGCCCCGGGAGCGCGTGCAGAGCCCCCGAAGCTG	3420
Db	3352	CCCCGGGAGACGCGCTGCGATGCGGACCCCGCCCCGGGAGCGCGTGCAGAGCCCCCGAAGCTG	3411

Qy	3421	CTGTGTCCGAGCTGGCGGAGATCCCGGGTACGCCATCGCCGGGGGTTCCGCTCAAC	3480
Db	3412	CTGGTGTCCGAGCTGGCGGAGATCCCGCATCGCCATTCGCCACGGCGTGCCTGTGAC	3471
Qy	3481	ACGGACTATTACTTCTCGCATCTCTCGGGGGCGGCTGCGTGAGTTCAAAGGCCCTGTTT	3540
Db	3472	ACGGACTATTACTTCTCCCACTGTTCGGGGCGCGTGCCTGACATTCAAAGGCCCTGTTT	3531
Qy	3541	GGAATAACGCGCAAGATCACCGAGAGTCTGTATAAGAGGTTTATTCGCCGAGAGCTGGCAC	3600
Db	3532	GGGAATAACGCCAAGATCACCGAGAGTCTGTATAAAGAGTTTATTCGCCAAGTGTGGCAC	3591
Qy	3601	CCCCCGGACGACGTGGCGCGCGGCTCAGAGCCGCGGGGTTCCGGCGCGCGGGGGCCGCG	3660
Db	3592	CCCCCGGACGACGTGGCGCGCGGCTCCGGGCGCAGGGTTCGGGGCGGTGGGGTCCGCGC	3651
Qy	3661	GCTACGCGGAGGAAACTCTCGAATGTTGCATAGAGCCTTTGATCTACTAGCATGA	3717
Db	3652	GCTACGCGGAGGAAACTCTCGAATGTTGCATAGAGCCTTTGATCTACTAGCATGA	3708

## RESULT 7

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US-10-692-556-5
; Sequence 5, Application US/10692556
; Publication No. US20040115623A1
; GENERAL INFORMATION:
; APPLICANT: Homa, Fred
; APPLICANT: Wathen, Michael
; APPLICANT: Hopkins, Todd
; APPLICANT: Thomsen, Darrell
; TITLE OF INVENTION: A Method for Treating Herpes Virus
; FILE REFERENCE: 00221
; CURRENT APPLICATION NUMBER: US/10/692,556
; CURRENT FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 3708
; TYPE: DNA
; ORGANISM: herpes simplex
US-10-692-556-5

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358	GGCGGCTTCTGGCGCGCGGCGTTCGGCGCTGTGGGGCGGCGGTGAGACACAGCCCGCGGGGG	417
421	TTCGACCCCAACGTCACCGTCTTCCACGTTGACGACATCTCGGAGCAGCTGGAAACAGCGC	480
418	TTCAACCCCAACGTCACCGTCTTTCACGTTGACGACATCTCGGAGAACGTTGGAGCAGCGC	477
481	TACAGCATGCGCGCGCGCCAGCTCCACGAGGGATTATGACGCCATACGCGCGCGCGG	540
478	TACGGCATGCGCGCGCGCCAGTTCCACGCGCGTTTATGACGCCATCACACGAGCGGG	537
541	ACCGTCATACGCTTCTGGGTCGTGACCCCGAAGGCCATCGCTCGCGGTTACAGTCTAC	600
538	ACCGTCATACGCTTCTGGGCTGACTCCGGAAGGCCACCGGGTGGCCGTTACAGTTTAC	597
601	GGCACGGCGAGTACTTTTATCATGAAACAAGCGGAGGTGATCGGCACCTGCAAGTGCCT	660
598	GGCACGGCGAGTACTTTTATCATGAAACAAGGAGGTTTCAGAGCACCTTACATGCCG	657
661	GCCCGCGCGATCTCTCGAGCGCTTGGCGGCGCCCTGCGGAGTTCGCGGGGGCGTGC	720
658	GCCCGACGAGATCTCTCGAGCGCATGCGCGCGCGCCCTGCGGAGTCCCGCGCGCGTGC	717
721	TTCCGCGGCATCTCCGCGGACCTTTCGAGCGGAGGTGTTGAGCGCGCGCGGACGTGTAC	780
718	TTCCGCGGCATCTCCGCGGACCTTTCGAGCGGAGGTGTTGAGCGGACCGAGACGTGTAC	777
781	TATTACAAACCGCGCCCGAACCTCTACTACCGGCTCTTCTGTGCGAAGCGGGCGCGGCTG	840
778	TACTACGAGCGCGCCCGCTCTGTTTTACCGGCTCTACGTCCGAAGCGGGCGGTGCTG	837
841	GCCTACCTGTGCGACAACATTTTCCCGCGCGATCAGGAAGTACGAGGGGGCGTGCAGCC	900
838	TCGTACCTGTGCGACAACATTTCTGCCCGGCATCAAGAAGTACGAGGGTGGGTGCGACGC	897
901	ACCACCGGTTTATCTGAGCAACCCGGGGTTTGTCACTTCCGCTGGTACCGCTCAAG	960
898	ACCAACCGGTTTATCTGAGCAACCCCGGGTTTGTCACTTCCGCTGGTACCGCTCAAA	957
961	CCGGCGCGCGGAAACGCGCGCGCCCAACCGCGCGCCCGACGCGCTTCGGAACTCGAGC	1020
958	CCGGCGCGGAACACACGCTAGCCGAGCGCGGGCCCCGATGCGCTTCGGGACATCCAGC	1017
1021	GAGTCGAGTTTAACTGCAACGGCGGAACAACCTGGCCGTGAGGGGGCCATGTGTGACCTG	1080
1018	GAGTCGAGTTTAACTGTAACGGCGGAACAACCTGGCCATCGAGGGGGGCATGAGCGACCTA	1077
1081	CCGGCTTACAAGCTCATGTGCTTCGATATCGAATCGAAGCCGGGGGGGAGGACGAGCTG	1140
1078	CCGGCATACAAAGCTCATGTGCTTCGATATCGAATGCAAGCGGGGGGGGAGGACGAGCTG	1137
1141	GCCTTTCGGTTCGGAAACGCCCGGAAGACCTCGTCAATCCAGATCTCTGTCTGCTCTAC	1200
1138	GCCTTTCGGTTCGGGCAACCCGAGGACCTGGTTATTACAGATATCTGTCTGCTCTAC	1197
1201	GACCTGTCCACCAACCGCCCTCGAGCACATCTCCTGTTTTTCGCTCGGATCTCTGCGACCTC	1260
1198	GACCTGTCCACCAACCGCCCTCGAGCACATCTCCTGTTTTTCGCTCGGATCTCTGCGACCTC	1257
1261	CCGAGTCCCACTCAGCGATCTCGGCTTCAGGGGCGCTGCGGCGCCCGCTGCTGTGGAG	1320
1258	CCGGAATCCCACTCAGCGATCTCGGCTTCGATATCGAATGCAAGCGGGGGGAGGACGAGCTG	1317
1321	TTTGTACAGCGAAATTCAGAGATGCTGTGGCTTTCATGACCTTCGTCAAGCAGTACGCGCCC	1380
1318	TTGTACAGCGAAATTCAGAGATGCTGTGGCTTTCATGACCTTGTGAAACAGTACGCGCCC	1377
1381	GAGTTGTGACCGGGTACAAATCATCAACTTCGACTGGCCCTTCGTCTCTGACCAAGCTG	1440
1378	GAGTTGTGACCGGGTACAAATCATCAACTTCGACTGGCCCTTCGTCTCTGACCAAGTGTG	1437
1441	ACGAGATCTACAAGGTCCGCTCGACGGGTACGGCGCATGAACGGCGGGGTGTGTTTC	1500
1438	ACGGACATTTACAAGTCTCCCTTGAACGGGTACGGCGCATGAACGGCGGGGTGTGTTT	1497



Qy	1501	CGCGTGGGACATCGGCGAGCCACTTTCAGAAAGCGCAGCAAGATCAAGGTGAACGGG	1560
Db	1498	CGCGTGGGACATAGGCCAGAGCCACTTCAGAAAGCGCAGCAAGATAAAGGTGAACGGC	1557
Qy	1561	ATGCTGAACATCGACATGTACGGATCATCAACGACAAAGGTCAAACTCTCCAGCTACAAG	1620
Db	1558	ATGCTGAACATCGACATGTACGGATCATCAACGACAAAGATCAAGCTCTCAGAGTACAG	1617
Qy	1621	CTGAACCGCGTCGCGGAGCGCTCTTGAAGGACAAGAAAGATCTGAGCTACCGGCAC	1680
Db	1618	CTCAACCGCGTGGCGGAAGCGCTCTTGAAGGACAAGAAAGAGACCTGAGCTATCGGCAC	1677
Qy	1681	ATCCCGCGCTACTAGCGCTCCGGGCGCGCAGCGCGGGGTGATCGGGAGTATTTGTG	1740
Db	1678	ATCCCGCGCTACTAGCGCGCGGCGCGCAACCGGGGTGATCGGGAGTACTGCATA	1737
Qy	1741	CAGACTCGCTGCTGGGCGAGCTGTTCTTCAAGTTTCTGCGCACCTCGAGCTTTCC	1800
Db	1738	CAGATTCCTTGTGTGGCCAGCTGTTTTTAAAGTTTTTGGCCCATCTGGAGCTCTCG	1797
Qy	1801	GCCGTGCGCGCTTGGGCGGATCAACATCAACCGCACCAATCTACGAGGCGCACGATC	1860
Db	1798	GCCGTGCGCGCTTGGGCGGTATTAACATCAACCGCACCAATCTACGAGGCGCACGATC	1857
Qy	1861	CGGCTCTTACGTGCTCTCGGCTTCGGGCGCAGAAAGGCTTCATCTGCGGCACACC	1920
Db	1858	CGGCTCTTACGTGCTCTCGGCTTCGGGCGCAGAAAGGCTTTATTTCTGCGGCACACC	1917
Qy	1921	CAGGGGCGTTTTCGGGGCTCGACAAAGAGCGGCCCAAGCGCCCGCGCTGCCCTCGGGG	1980
Db	1918	CAGGGGCGATTTAGGGGCGCGGGGGAGGCGCCCAAGCGTCCGGCGCAGCCCGGGAG	1977
Qy	1981	GAAGGGAGCGCGGGGACGGGAAACGGGACAGAGGATAAGGACGACGAGGACGAG	2040
Db	1978	GACGAGGAGCGCGAGGAGGAGGGGAGGAGC-----AGGACGAACGAGGAGGGC	2031
Qy	2041	GACGGGACGAGCGGAGGAGGTTCGCGCGAGACCGGGGCGCGACGTTGGGTACGAG	2100
Db	2032	GGGGCGAGCGGAGCGGAGGCGCGGGAGACCCGCGCGCGGACGTGGGGTACCGAG	2091
Qy	2101	GGGGCGGGTCTTCGACCCACCTTCGGGTTTACGTCGACCCCGTGGTGTGTTTGAC	2160
Db	2092	GGGGCGAGGTTCTTGACCCCACTTCGGGTTTACGTGAACCCCGTGGTGTGTTTGAC	2151
Qy	2161	TTTGCAGCTGTATCCCAAGCATCATCCAGGCGCCACCAACCTGTGCTTCAGTACGCTCC	2220
Db	2152	TTTGCAGCTGTATCCCAAGCATCATCCAGGCGCCACCAACCTGTGCTTCAGCACGCTCTCC	2211
Qy	2221	CTGCGGCGGAGCGCTTCGCGACCTTGAGGGGACCGGGACTACCTGGAGATCGAGTG	2280
Db	2212	CTGAGGGCGGACGAGTGGCGACCTTGAGGGGCGGCAAGGACTACCTGGAGATCGAGTG	2271
Qy	2281	GGGGCGGACGCGTCTTCTGTGAAGCCCAAGTACGCGAGAGCTCTCTCAGAGATCTG	2340
Db	2272	GGGGGCGACGCGTCTTCTGTGAAGCTCACGTGCGAGAGGCTCTCTCAGAGATCTCTC	2331
Qy	2341	CTGCGGAGTGGCTGGCCATCGAAAGCAGATTCGCTCGCGGATCCCCCAGAGCACCCCC	2400
Db	2332	CTGCGGAGTGGCTGGCCATCGAAAGCAGATTCGCTCGCGGATTTCCCCCAGAGCACCCCC	2391
Qy	2401	GAGAGGCGCTCTCTCTCGACAGCAACAGCGCGGCATCAAGGTGGTGTGCAATCTCGTG	2460
Db	2392	GAGAGGCGCTCTCTCTCGACAGCAGAGCGCGGCATCAAGGTGGTGTGCAATCTCGTG	2451
Qy	2461	TACGGTTTACCGGGCGCAGCAGCTCTCTGCGCTGCGCTGCGCTGCGCCACCGTG	2520
Db	2452	TACGGTTTACCGGGAGCGAGCAGGACTCTCTGCGCTGCGCTGCGCTGCGCCAGCGTG	2511
Qy	2521	ACGACCATCGGCGCGAGATGCTCTCTCGCAGCGCGCGCTCGTGACCGCGCTGGGCG	2580
Db	2512	ACGACCATCGGCGCGAGATGCTGCTCGCGACCCCGCAGGATCGTCCACGCGCGCTGGGCG	2571

Qy	2581	GAGTTCGATCAGCTGCTGGCGGACTTTCCGAGGCGCGCGCATGCGCGCCCCCGGTCCG	2640
Db	2572	GCCTTCGAAACAGCTTCCTGGCCGATTTCCGAGGCGCGCGACATGCGGGCCCCCGGGCC	2631
Qy	2641	TACTCCATGGGCATCATCTACGGGACACAGGACTCCATTTTTCGTTTGTGCGCGGCTC	2700
Db	2632	TATTCATGCGCATCATCTACGGGACACAGGACTCCATATTTGTGCTGTGCGCGGCTC	2691
Qy	2701	ACGGCCCGGCGCTGTGGCATATGGGCGACAAGATGGGAGCGACATCTCGCGCGCGCTG	2760
Db	2692	ACGGCCCGGCGGTGACGGGCATGGGCGACAAGATGGGAGCCACATCTCGCGCGCGCTG	2751
Qy	2761	TTCTCTCCCGCATCAAGCTCGAGTGCAGAAAACGTTTCCAAAGCTGCTCATCGGCC	2820
Db	2752	TTTCTGCCCCCATCAAACTCGAGTGCAGAAAAGAGCTTCAACAGCTGCTGCTCATCGCC	2811
Qy	2821	AAGAAAAAGTACATCGGCGCTCATCTGCGGGGCAAGATGCTCATCAAGGGCGTGGATCTG	2880
Db	2812	AAGAAAAAGTACATCGGCGCTCATCTA CGGGGTAAAGATGCTCATCAAGGGCGTGGATCTG	2871
Qy	2881	GTGGCGAAAAACAACTCGGCGTTTATCAACCGACCTCCAGGGCCCTGCTCGACTGCTG	2940
Db	2872	GTGGCGAAAAACAACTCGGCGTTTATCAACCGACCTCCAGGGCCCTGCTCGACTGCTG	2931
Qy	2941	TTTTTACGACGATACCGTATCCGAGCGCGCGCGCTTAGCCGAGCGCCCCCGCAGAGGAG	3000
Db	2932	TTTTTACGACGATACCGTATCCGAGCGCGCGCGCTTAGCCGAGCGCCCCCGCAGAGGAG	2991
Qy	3001	TGGTGGCGGACCCCTGCGCGGAGGAGCTGCGAGCGTTTGGGGCGCTCTCGTAGAGGCC	3060
Db	2992	TGGTGGCGGACCCCTGCGCGGAGGAGCTGCGAGCGTTTGGGGCGCTCTCGTAGAGGCC	3051
Qy	3061	CATCGGCGCATACCGACCGGAGAGGAGCATCAGAGCTTTTGTCTTCACCGCGCACTG	3120
Db	3052	CATCGGCGCATACCGACCGGAGAGGAGCATCAGAGCTTTTGTCTTCACCGCGCACTG	3111
Qy	3121	AGCAGACCCCGCGCGGTACACCAACGCGCTGCGCCACCTGAGCGTGTATTACAAAG	3180
Db	3112	AGCAGACCCCGCGCGGTACACCAACGCGCTGCGCCACCTGAGCGTGTATTACAAAG	3171
Qy	3181	CTCATGCGCGCGCGCGCGAGTCCGCTCCATCAAGGACCGGATCCCGTACGTGATCGTG	3240
Db	3172	CTCATGCGCGCGCGCGCGAGTCCGCTCCATCAAGGACCGGATCCCGTACGTGATCGTG	3231
Qy	3241	GCCAGACCCCGCGAGGTAGAGGAGACGCTCGCGCGCTGGCGCGCTCCGCGAGCTAGAC	3300
Db	3232	GCCAGACCCCGCGAGGTAGAGGAGACGCTCGCGCGCTGGCGCGCTCCGCGAGCTAGAC	3291
Qy	3301	GCCGCGCGCCAGGGGACGAGCGCGCCCCCAGCGGCGCTTCCCTCCCGGCGCAAGGCG	3360
Db	3292	GCCGCGCGCCAGGGGACGAGCGCGCCCCCAGCGGCGCTTCCCTCCCGGCGCAAGGCG	3351
Qy	3361	CCCCGGGAGACGCGCTCGCATGCGCACCCCCCGGGAGCGCGTCCAAAGCCCCGCAAGGTG	3420
Db	3352	CCCCGGGAGACGCGCTCGCATGCGCACCCCCCGGGAGCGCGTCCAAAGCCCCGCAAGGTG	3411
Qy	3421	CTGTGTCCGAGCTGGCGGAGGATCCCGGTTACGCGCATCGCGCGGGGCTTCCGCTCAAC	3480
Db	3412	CTGTGTCCGAGCTGGCGGAGGATCCCGGTTACGCGCATCGCGCGGGGCTTCCGCTCAAC	3471
Qy	3481	ACGAGCTATTACTTCTCGCACTCTGGGGGCGGCTTGCCTGAGCTTCAAGGCGCTGTTT	3540
Db	3472	ACGAGCTATTACTTCTCCACCTTGTGGGGGCGGCTGCTGACATTCAGAGGCTGTTT	3531
Qy	3541	GGAAATACGCAAGATCACCGAGAGTCTGTTAAAGAGGTTTATTCGCGAGACGTTGGAC	3600
Db	3532	GGGAATACGCAAGATCACCGAGAGTCTGTTAAAGAGGTTTATTCGCGAGTGTGGAC	3591
Qy	3601	CCCCCGGAGAGCTGGCGCGCGGCTCAGGGCGCGGGGTTTCGGGCGCGCGGGCGCGGC	3660
Db	3592	CCCCCGGAGAGCTGGCGCGCGGCTCAGGGCGCGGGGTTTCGGGCGCGCGGGCGCGGC	3651
Qy	3661	GCTACGGCGAGGAAACTCGTCGAATGTTGCTAGAGCGCTTTTGATCTTAGCATGA	3717

Db 3652 GCTACGGCGGAGAAATCTGTCGAATGTTGCATAGAGCCTTTGATCTCTAGCATGA 3708

## RESULT 8

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US-09-904-065-7
; Sequence 7, Application US/09904065
; Patent No. US20020076789A1
; GENERAL INFORMATION:
; APPLICANT: Homa, Fred
; APPLICANT: Wathen, Michael
; APPLICANT: Hopkins, Todd
; APPLICANT: Thomsen, Darrell
; TITLE OF INVENTION: A Method for Treating Herpes Virus
; FILE REFERENCE: 00221
; CURRENT APPLICATION NUMBER: US/09/904.065
; CURRENT FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 3708
; TYPE: DNA
; ORGANISM: herpes simplex
US-09-904-065-7

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Query Match 82.1%; Score 3053.4; DB 9; Length 3708;  
Best Local Similarity 89.2%; Pred. No. 0;  
Matches 3317; Conservative 0; Mismatches 391; Indels 9; Gaps 2

Qy	1	ATGTTTGTGCGGGGCGGCGCCGACNTCTCCCGGGGGGAAGTCGGCGGCTCGGGCGCG	60
Db	1	ATGTTTTCGGGTGGCGGGCGGCGCTGTCTCCCGGAGGAAAGTCGGCGGCAAGGGCGCG	60
Qy	61	TCGGGGTTTTTGTGCCCCCAAAACCCCGGGGAGCCACCAGACGGCACCGCGGCTTTGC	120
Db	61	TCGGGGTTTTTGTGCGCGCGCGCCCTCGCGGAGCGGCG---GGGGACCCCGGCTTTGC	117
Qy	121	GCGCGGAGAACTTCTACAACCCCCCACTCTGCTCAGACCGGAAACGACGACCAAGGCCCCC	180
Db	118	TTGAGGCAAAACTTTTACAACCCCTACTCTGCCCCAGTCGGGAGCGCAACAGAAGCGGACC	177
Qy	181	GGGCGGCTCAGCGCCATACGTACTACAGCAGATGCGACGAATTTTCGATTTTATCGCCCG	240
Db	178	GGGCAACCAACGCGCATACGTAATTATACGAATGCGATGAATTCGATTTTATCGCCCG	237
Qy	241	CGTTCGTGACAGAGACGCCCCCGCGAGACGCGACCGGGGTCACGACGGCGCGCTC	300
Db	238	CGGGTGCTGGACGAGGATGCCCCCGGAGAAAGCGCGCGGGTGCAAGACGCTCACCTC	297
Qy	301	CGGCGCGCCCTAAGGTGTACTGCGGGGGGACGAGCGGACGTCCTCGCGGTGGGCGCG	360
Db	298	AAGCGCGCCCCAAGGTGTACTGCGGGGGGACGAGCGGACGTCCTCGCGGTGGGGTCG	357
Qy	361	GAGGCTTCTGGCGCGCTGCGCTGTGGGCGGTCGGGACCATGCCCCCAAGGGG	420
Db	358	GGCGGCTTCTGGCGCGGGGCTCGGGCTGTGGGCGGCTGGACCAAGCGCGCGGGG	417
Qy	421	TTGACCCCAACCGTCAACCGTCTTCCAAGTGTACGACATCTTGGAGCAAGTGGAAACAGCG	480
Db	418	TTCAACCCCAACCGTCAACCGTCTTTCACGTTGTACGACATCTTCGAGAAAGTGGAGCACGCG	477
Qy	481	TACAGCATGCGCGCGGCCAGCTCCACGAGCGATTTATGGACGCATCACGCGCGCGCGG	540
Db	478	TACGGCATGCGCGCGGCCAGTTTCAACGCGGGTTTATGGACGCCATCACCGACGGGG	537
Qy	541	ACCGTCATACGCTTCTGGGTCTGACCCCGAAGGCCATCGCGTTCGCGGTTTACGCTTAC	600
Db	538	ACCGTCATACGCTCTGGGCTGACTCCGGAAGGCCACCGGTTGGCGCTTTCACGTTTAC	597
Qy	601	GGACGGCGGAGTACTTTTATGAACAAAGCGGAGGTGGATGGGCACTGCAGTGCCGT	660
Db	598	GGACGGCGGAGTACTTTTATGAACAAAGAGAGAGTTCGACAGGCACTTCAATTCGCGC	657



[illegible]

Db	2812	AAGAAAAGTACATCGCGCTCATCTACGGGGTAAAGATGCTCATCAAGGCGCTGGAATCTG	2871
Qy	2881	GTGCGCAAAAACAACTCGCGCTTTATCAACCGCACCTTCAAGGGCCCTGGTCGACCTGCTG	2940
Db	2872	GTGCGCAAAAACAACTCGCGCTTTATCAACCGCACCTTCAAGGGCCCTGGTCGACCTGCTG	2931
Qy	2941	TTTTACGACGATACCGTATCCGAGGCGCGCGCTTACGCGAGCGCCCGCAGAGGAG	3000
Db	2932	TTTTACGACGATACCGTATCCGAGGCGCGCGCTTACGCGAGCGCCCGCAGAGGAG	2991
Qy	3001	TGGCTGCGCGACCCCTGCCCCGAGGAGACTCAGCGCTTGGGGCCGCTCTCTGTAGACGCC	3060
Db	2992	TGGCTGCGCGACCCCTGCCCCGAGGAGACTCAGCGCTTGGGGCCGCTCTCTGTAGACGCC	3051
Qy	3061	CATCGGCGCATACCGACCCGAGAGGAGCATCAGGACTTTGTCTCTCAACCGCCGAACTG	3120
Db	3052	CATCGGCGCATACCGACCCGAGAGGAGCATCAGGACTTTGTCTCTCAACCGCCGAACTG	3111
Qy	3121	AGCAGACACCGCGCGGTACACCAACAGCGCTTGGCCCACTGACGGTGTATTACAAG	3180
Db	3112	AGCAGACACCGCGCGGTACACCAACAGCGCTTGGCCCACTGACGGTGTATTACAAG	3171
Qy	3181	CTCATGCCCCCGCGCGCAGGCTCCGCTCCATCAAGGACCGGATCCCGTACGTGATCGTG	3240
Db	3172	CTCATGCCCCCGCGCGCAGGCTCCGCTCCATCAAGGACCGGATCCCGTACGTGATCGTG	3231
Qy	3241	GCCCAGACCCGCGAGGTAGAGGAGAGCGTTCGCGCGCTTGGCCGCTTCGCGAGCTTAGAC	3300
Db	3232	GCCCAGACCCGCGAGGTAGAGGAGAGCGTTCGCGCGCTTGGCCGCTTCGCGAGCTTAGAC	3291
Qy	3301	GC CGCGCCCCAGGGAGAGCGCGCCCCCGCAGCGGCTTCGCTCCCGGCCAAGCGC	3360
Db	3292	GC CGCGCCCCAGGGAGAGCGCGCCCCCGCAGCGGCTTCGCTCCCGGCCAAGCGC	3351
Qy	3361	CCC CGGAGACGCGCTCGCATGCGACCCCCCGGAGCGCGTCCAAGCCCCCGCAAGCTG	3420
Db	3352	CCC CGGAGACGCGCTCGCATGCGACCCCCCGGAGCGCGTCCAAGCCCCCGCAAGCTG	3411
Qy	3421	CTGGTGTCCGAGTGGCGGAGGATCCGGGTAGCCATCGCCCGGGGGCTTCGGCTCAAC	3480
Db	3412	CTGGTGTCCGAGTGGCGGAGGATCCGGGTAGCCATCGCCCGGGGGCTTCGGCTCAAC	3471
Qy	3481	ACGGACTATTACTTCTCGACCTGTCTGGGGCGGCGCTGGCTGACGTTCAAGGCCCTGTGTT	3540
Db	3472	ACGGACTATTACTTCTCGACCTGTCTGGGGCGGCGCTGGCTGACGTTCAAGGCCCTGTGTT	3531
Qy	3541	GGAAATAACGCCAAGATCACCGAGAGTCTGTTAAAGAGGTTTATTCGCGAGACGTGGCAC	3600
Db	3532	GGAAATAACGCCAAGATCACCGAGAGTCTGTTAAAGAGGTTTATTCGCGAGACGTGGCAC	3591
Qy	3601	CCCCCGGACGAGCTGGCGCGCGGCTCAGGGCCGCGGGGTTGGGGCGCGCGGGGCGCGC	3660
Db	3592	CCCCCGGACGAGCTGGCGCGCGGCTCAGGGCCGCGGGGTTGGGGCGCGCGGGGCGCGC	3651
Qy	3661	GCTACGCGGAGGAAACTCGTCAAAATGTTGSCATAGAGCCCTTGTATCTCTAGCATGA	3717
Db	3652	GCTACGCGGAGGAAACTCGTCAAAATGTTGSCATAGAGCCCTTGTATCTCTAGCATGA	3708

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RESULT 9
US-10-692-556-7
; Sequence 7, Application US/10692556
; Publication No. US20040115623A1
; GENERAL INFORMATION:
; APPLICANT: Homa, Fred
; APPLICANT: Mathen, Michael
; APPLICANT: Hopkins, Todd
; APPLICANT: Thomsen, Darelle
; TITLE OF INVENTION: A Method for Treating Herpes Virus
; FILE REFERENCE: 00221
; CURRENT APPLICATION NUMBER: US/10/692,556
; CURRENT FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 19

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Qy	2041	GACGGGACGAGCCGCGAGAGAGTTCGCGCGCGAGACCGGGGGCCCGACAGCTTGGGTACCAG	2100
Db	2032	GGGGGCGAGCGGAGCCGCGAGGGCGCGCGGAGACCGCGCGCGCGACAGCTGGGGTACCAG	2091
Qy	2101	GGGGCCCGGGTCTCGACCCACCTCCGGGTTCACGTCGACCCCGTGGTGGTGTTCAC	2160
Db	2092	GGGGCAGGGTCTTGAACCCACATTCCTGGGTTCATGTGAACCCGTGGTGGTTCGAC	2151
Qy	2161	TTTGCCAGCCTGTATCCCCAGCATCATCCAGGCCCAACAACTGTCTTCAGTACGCTCTCC	2220
Db	2152	TTTGCCAGCCTGTATCCCCAGCATCATCCAGGCCCAACAACTGTCTTCAGTACGCTCTCC	2211
Qy	2221	CTGCGGCGCGAGGGCGTTCGGCACCTCGAGCGGACCGGGACCTACTGAGATTCGAGGTC	2280
Db	2212	CTGAGGGCCGACGCGAGTGGCGCACCTCGAGCGCGGCAAGACTACTCGGAGATCGAGGTC	2271
Qy	2281	GGGGGCGACGGCTGTTCTTCGTGAAGGCCCAAGTACGCGAGAGCCTGCTGAGCATCTCTG	2340
Db	2272	GGGGGCGACGGCTGTTCTTCGTCAAGGCTCAAGTGCAGAGAGCCTCTCAGCATCTCTC	2331
Qy	2341	CTGCGGACCTGGCTGGCGCATCGGAAGAGAGATCGCTCGCGGATCCCGCCAGAGACCCCC	2400
Db	2332	CTGCGGACCTGGCTCGCGCATCGGAAGAGAGATCGCTCGCGGATCCCGCCAGAGACCCCC	2391
Qy	2401	GAGGAGCGCTCTCTCGACAGACACAGCGCGCCATCAAGTGGTGTGCAACTCGGTG	2460
Db	2392	GAGGAGCGCTCTCTCGACAGAGACAGCGCGCCATCAAGTGTGTGTAACTCGGTG	2451
Qy	2461	TACGGGTTCACCGGGGCGACAGCGTCTTCTGCGCTGCCCTGACGCTGGCGCGCACCGCTG	2520
Db	2452	TACGGGTTCACCGGAGCGCAGCAGGACTCTCTGCGCTGCCCTGACGCTGGCGCGACCGCTG	2511
Qy	2521	ACGACCATCGGCGCGAGATGCTCCTCGACAGCGCGCGGTACGTGCACGCGCGCTGGGCG	2580
Db	2512	ACGACCATCGGCGCGAGATGCTCTCGACAGCGCGCGGTACGTGCACGCGCGCTGGGCG	2571
Qy	2581	GAGTTCGATCAGCTGCTGGCGGACTTTCGAGGCGCGGACATGCGCGCGCCCGGCTCG	2640
Db	2572	GCCTTCGACAGCTCTCTGGCGGATTTCCGGAGGCGCGACATGCGCGCGCCCGGCGCC	2631
Qy	2641	TACTCCATGGGCATCATCTACGGGACACCGGACTTCATTTTGTGTGTGTCGCGCGGCTC	2700
Db	2632	TATTCCATGGGCATCATCTACGGGACACCGGACTTCCATTTGTGTGTGTCGCGCGGCTC	2691
Qy	2701	ACGCGCGCGGCGTGGTCATGGGCGACAGATGCGGAGCCACATCTCGCGCGGCTG	2760
Db	2692	ACGCGCGCGGCGTGA CGGCGTGGGCGACAGATGCGGAGCCACATCTCGCGCGGCTG	2751
Qy	2761	TTCTCTCCCGCGATCAAGCTCGAGTGGGAAAAAGCTTACCAAGCTGCTGCTCATCGCC	2820
Db	2752	TTTCTGTCCCCCATCAAACTCGAGTGGGAAAAAGCTTACCAAGCTGCTGCTCATCGCC	2811
Qy	2821	AAGAAAAAGTACATCGGCGTCATCTCGGGGGGCAAGATGCTCATCAAGGCGTGGATCTG	2880
Db	2812	AAGAAAAAGTACATCGGCGTCATCTA CGGGGGTAAAGTGTCTCATCAAGGCGTGGATCTG	2871
Qy	2881	GTGCGCAAAACAACTGCGCGTTTATCAACGCGACCTCCAGGGCGCTGCTCGACCTGCTG	2940
Db	2872	GTGCGCAAAACAACTGCGCGTTTATCAACGCGACCTCCAGGGCGCTGCTCGACCTGCTG	2931
Qy	2941	TTTTTACGACGATACCGTATCCGAGCGCGCGCGCTTACCGAGCGCCCGCGAGAGAG	3000
Db	2932	TTTTTACGACGATACCGTATCCGAGCGCGCGCGCTTACCGAGCGCCCGCGAGAGAG	2991
Qy	3001	TGGCTGGCGGACCCCTCGCGGAGGACTGACAGCGTTTCGGGGCGTCTCGGTAGACGCC	3060
Db	2992	TGGCTGGCGGACCCCTCGCGGAGGACTGACAGCGTTTCGGGGCGTCTCGGTAGACGCC	3051
Qy	3061	CATCGGCGCATCACCGACCCGGAGAGGAGATCCAGGACTTTGTCTCTCACCGCGGAACTG	3120
Db	3052	CATCGGCGCATCACCGACCCGGAGAGGAGATCCAGGACTTTGTCTCTCACCGCGGAACTG	3111

QY	3121	AGCAGACACCGCGCGGTACACPAACAGCGCTGGCCCACTGACGGTGATTTACAAG	3180
DB	3112	AGCAGACACCGCGCGGTACACPAACAGCGCTGGCCCACTGACGGTGATTTACAAG	3171
QY	3181	CTCATGCGCCGCGCGAGGTCCGTCATCAAGACCGGATCCGTCACGTGATCGTG	3240
DB	3172	CTCATGCGCCGCGCGCGAGGTCCGTCATCAAGACCGGATCCGTCACGTGATCGTG	3231
QY	3241	GCCCAGACCGCGAGGTAGGAGACGGTCGCGCGCTGGCCGCTCCGCGAGCTAGAC	3300
DB	3232	GCCCAGACCGCGAGGTAGGAGACGGTCGCGCGCTGGCCGCTCCGCGAGCTCGAC	3291
QY	3301	GCGCGCGCCCAAGGGACGAGCCGCCCCCAAGCGGCCCTGCGCTCCCGGCCAAGCGC	3360
DB	3292	GCGCGCGCCCAAGGGACGAGCCGCCCCCAAGCGGCCCTGCGCTCCCGGCCAAGCGC	3351
QY	3361	CCCCGGGAGACCGTCGCATGCCAGCCCCCGGGAGGCGCGTCAAGCCCGCCGAAGCTG	3420
DB	3352	CCCCGGGAGACCGCTTGCATGCCAGCCCCCGGGAGGCGCGTCAAGCCCGCCGAAGCTG	3411
QY	3421	CTGGTGTCGAGCTGGCGGAGGATCCCGGGTACGCCATCGCCCGGGCGCTTCGCGTCAAC	3480
DB	3412	CTGGTGTCGAGCTGGCGGAGGATCCCGGGTACGCCATCGCCCGGGCGCTTCGCGTCAAC	3471
QY	3481	ACGGACTATTACTCTCGCATCTGTGGGGCGGCCCTGGCTGACGTTCAAGGCCCTGTTT	3540
DB	3472	ACGGACTATTACTCTCGCATCTGTGGGGCGGCCCTGGCTGACATCAAGGCCCTGTTT	3531
QY	3541	GGAATAACCCAGATCACCGAGAGTCTGTAAAGAGGTTTATTCGCCGAGCGTGGCAC	3600
DB	3532	GGAATAACCGCAAGATCACCGAGAGTCTGTAAAGAGGTTTATTCGCCGAGTGGGCAC	3591
QY	3601	CCCCCGGACGACGTGGCGCGCGCTCAGGGCCCGCGGGTTCGGGCGGGCGGGCGCGC	3660
DB	3592	CCCCCGGACGAGTGGCGCGCGCTCAGGGCCCGCGGGTTCGGGCGGGTGGGTGGCGC	3651
QY	3661	GCTACGCGGAGGAACCTCTCGAAATGTTGCATAGAGCCCTTGATATCTTAGCATGA	3717
DB	3652	GCTACGCGGAGGAACCTCTCGAAATGTTGCATAGAGCCCTTGATATCTTAGCATGA	3708

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RESULT 10
US-09-904-065-9
; Sequence 9, Application US/09904065
; Patent No. US20020076789A1
; GENERAL INFORMATION:
; APPLICANT: Homa, Fred
; APPLICANT: Wathen, Michael
; APPLICANT: Hopkins, Todd
; APPLICANT: Thomsen, Darrell
; TITLE OF INVENTION: A Method for Treating Herpes Virus
; FILE REFERENCE: 00221
; CURRENT APPLICATION NUMBER: US/09/904,065
; CURRENT FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 3708
; TYPE: DNA
; ORGANISM: herpes simplex
US-09-904-065-9

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	Query Match	82.0%	Score 3047;	DB 9;	Length 3708;
	Best Local Similarity	89.1%	Pred. NO. 0;		
	Matches 3313;	Conservative 0;	Mismatches 395;	Indels 9;	Gaps 2;
Qy	1	ATGTTTGTGCGCGCGCGCCGAC	TTCCCCCGGGGGGAAGTCGCGCGGCTCGGCGCGCG	60	
		1	ATGTTTCCGCTGCGCGCGCGCGCTG	CCCCCGAGGAAGTCGCGCGGCGGCGCGCG	60
Db					
Qy	61	TCCTCGGTTTTTTTGGCCCCCACA	CCCCCGGGGAGCCACCAGACGGGACCGCGCGCCTTGC	120	
Db	61	TCCGGTTTTTTTGGCGCGCGCGCGCCCTCGCGGAGCGGGC	---GGGAGACCCCGCGCTTGT	117	

QY 121 CCGCGGAGAGCTTCTACAACCCCACTCGCTCAGACCGGAAACGAGCAAGGCCCGC 180  
DB 118 TTGAGGCAAAACTTTTACAACCCCTACCTCGCCCAAGTCGGAGCGCAACAGAGCGGACC 177  
QY 181 GGGCGGCTCAGCGGCATAGCTACTACAGCGAGTGGAGCAATTTTCGATTTATCGCCCG 240  
DB 178 GGGCAACCCAGCGGCATAGCTACTATAGCGAATGCGATGAATTTTCGATTTATCGCCCG 237  
QY 241 CGTTTCGCTGAGAGAGAGCGCCCGCGAGCAGCGCACCGGGGTCCACGACCGCGCCCTC 300  
DB 238 CGGGTGTGAGAGAGATGCCCGCGGAGAGCGCGCGGGTGCACAGCGTCACTCTC 297  
QY 301 CGCGCGCCCTTAAGTGTATCTGCGGGGGAGAGCGCGAGTCTCTCGCGTGGGCGCG 360  
DB 298 AAGCGCGCCCAAGAGTGTACTGCGGGGGAGAGCGCGAGTCTCTCGCGTTCGGGTG 357  
QY 361 GAGGGCTTTCGCGCGGCTCGCTTGCCTGTGGGGGGTGGCGACATGCCCCCAAGGGG 420  
DB 358 GCGGCTTTCGCGCGGCGCTCGCGCTGTGGGGGGAGAGCGCGAGTCTCTCGCGTTCGGGTG 417  
QY 421 TTTCGACCCCAACCGTCAACCGTCTTCAACGTGTACGACATCTTCGAGCAGCTGGAACACGCG 480  
DB 418 TTCAACCCCAACCGTCAACCGTCTTTCAGGTGTATGACATCTTCGAGAAAGTGGAGCAGCG 477  
QY 481 TACAGATGCGCGCCCGCAGCTCCACAGCGATTTATGAGCGCCATCACCGCCCGCGGG 540  
DB 478 TACGGCATGCGCGCGCCAGTTCCACGCGCGGTTTATGAGCGCCATCACACCGAGGGG 537  
QY 541 ACCGTATCATCAGCTTCTGGTCTGACCCCGAAGGCGATTCGGTTCGGCGTTCACGTCTAC 600  
DB 538 ACCGTATCATCAGCTTCTGGTCTGACCTCGGAAAGGCGACCGGGTGGCGTTCACGTTTAC 597  
QY 601 GGCAGCGGCGAGTCTTTTACATGAACAGCGGAGGTGATTCGCGACCTTCAGTGGCGT 660  
DB 598 GGCAGCGGCGAGTCTTTTACATGAACAGGAGGAGGTGACAGGCACTTCAATAGCCGC 657  
QY 661 GCGCGCGGATCTCTGCGAGCGCTTGGCGGCGCTTGGCGAGTTCGCGAGTTCGCGGGCGGTG 720  
DB 658 GCGCGCGGATCTCTGCGAGCGATGCGCGCGCTTGGCGAGTTCGCGGGCGGTG 717  
QY 721 TTCGCGGATCTCTGCGAGCACCTTCGAGGCGAGGTGGTGGAGCGCGCGACGTGTAC 780  
DB 718 TTCGCGGATCTCTGCGAGCACCTTCGAGGCGAGGTGGTGGAGCGCACCGACGTGTAC 777  
QY 781 TATTACGAAACGCGCGGACCTGTACTACCGGCTTTCGTCGAAAGCGGCGCGCTG 840  
DB 778 TACTACGAGACGCGCGGCTGTGTTTACCGGCTTACGTCGAAAGCGGCGGCTGTG 837  
QY 841 GCCTACCTGTGCGACAACTTTTGCCTCGCGATCAGGAAAGTACGAGGGGGGTTCGACGCC 900  
DB 838 TCGTACCTGTGCGACAACTTTGCTGCGCGCATCAAGAGTACGAGGTGGGGTTCGACGCC 897  
QY 901 ACCACCGGTTATCTCGAGCAACCCCGGGTTTGTACCTTCGCGGTGTATCGCGCTCAAG 960  
DB 898 ACCACCGGTTATCTCGAGCAACCCCGGGTTTGTACCTTCGCGGTGTATCGCGCTCAAA 957  
QY 961 CCGCGCGGGAACGCGCGGCGCAACCGCGCGCGCGCGCGGCTTCGGAACCTTCGAGC 1020  
DB 958 CCGGCGGGAACAACAGCTAGCCCGCGCGCGCGCGCGGCTTCGGAACATTCAGC 1017  
QY 1021 GACGTCGAGTTTAACTGACGCGCGCAACCTTGGCGCTCGAGGGGGCGCATGTGTGACCTG 1080  
DB 1018 GATGTCGAGTTTAACTGACGCGCGCAACCTTGGCGCATCGAGGGGGCATGAGCGACCTA 1077  
QY 1081 CCGGCTTACAGCTCATGTGCTTCGATATCGAATCGAAGCGCGGGGGAGAGAGAGCTG 1140  
DB 1078 CCGGCTTACAGCTCATGTGCTTCGATATCGAATCGAAGCGGGGGAGAGAGAGCTG 1137  
QY 1141 GCCTTTCGCGTTCGCGGAACCGCGGAGACCTCGTCATCCAGATCTCTGCTCTAC 1200  
DB 1138 GCCTTTCGCGTTCGCGGAGACCGCGGAGACCTGCTCATCCAGATATCTGCTCTAC 1197

QY 1201 GACCTGTCCACACCGCGCTTCGAGCACATCTCTGTTTTCGTCGGATCTCGACCTC 1260  
DB 1198 GACCTGTCCACACCGCGCTTCGAGCACATCTCTGTTTTCGTCGGATCTCGACCTC 1257  
QY 1261 CCGAGTCCCACTCAGCGATCTCGCTCCAGGGGCTTCGCGCGCGCTTCGTCCTGAG 1320  
DB 1258 CCGGAATCCCACTCAGCGATCTCGCGCGCAGGGGCTTCGCCACCGCTGCTTCTGGAA 1317  
QY 1321 TTTCACGCGAATTCGAGATCTGCTGGCTTCATGACCTTCGTCGTCGTCGTCGTCG 1380  
DB 1318 TTTCACGCGAATTCGAGATCTGCTGGCTTCATGACCTTCGTCGTCGTCGTCGTCG 1377  
QY 1381 GAGTTGTCGACCGGTACAAATCATCACTTCGACCTTCGTCGTCGTCGTCGTCGTCG 1440  
DB 1378 GAGTTGTCGACCGGTACAAATCATCACTTCGACCTTCGTCGTCGTCGTCGTCGTCG 1437  
QY 1441 ACGGAGATCTACAGGTCTCGCTCGACGGGTACGGGCGCATGAACGGCGGGGTGTTTC 1500  
DB 1438 ACGGACATTTTACAAGGTCTCGCTCGACGGGTACGGGCGCATGAACGGCGGGGTGTTTC 1497  
QY 1501 CGCGTTCGGACATCGCGCGAGGCGCTTCGAGAGCGCAGCAAGATCAAGGTGAACGGG 1560  
DB 1498 CGCGTTCGGACATAGGCGCAGGCGCTTCGAGAGCGCAGCAAGATCAAGGTGAACGGG 1557  
QY 1561 ATGTTGAATCGAATGTACGGCATCATCAACGCAAGGTCAAACTCTCCAGCTACAAG 1620  
DB 1558 ATGTTGAATCGAATGTACGGCATCATCAACGCAAGATCAAGCTCTCGAGCTACAAG 1617  
QY 1621 CTGAACCGCGTTCGCGAGCGCTCTTGAAGGACAAGAAAGAGATCTGAGCTACCGGAC 1680  
DB 1618 CTGAACCGCGTTCGCGAGCGCTCTTGAAGGACAAGAAAGAGATCTGAGCTATCGGAC 1677  
QY 1681 ATCCCGCTACTACGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1740  
DB 1678 ATCCCGCTACTACG 1737  
QY 1741 CAGGATCTGCTGCTGCTGCGCGCGAGCTGTTCTTCAAGTTTCTGCCACCTCGAGCTTTC 1800  
DB 1738 CAGGATCTGCTGCTGCTGCGCGCGAGCTGTTTAAAGTTTTCGCCCATCTCGAGCTTCG 1797  
QY 1801 GCGTTCGCGCGCTTCGCGGGGATCAACATACCGCGCACCTTACGAGCGCGCAGATC 1860  
DB 1798 GCGTTCGCGCGCTTCGCGGGGTATTAACATCACCGCACCTTACGAGCGCGCAGATC 1857  
QY 1861 GCGTTCGCTTCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1920  
DB 1858 GCGTTCGCTTCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1917  
QY 1921 CAGGGCGGTTTCGCGGGCTTCGACAAAGAGCGCGCGCGCGCGCGCGCGCGCGCG 1980  
DB 1918 CAGGGCGGTTTACGGGCGCGCGGGGGAGCGCGCGCGCGCGCGCGCGCGCGCG 1977  
QY 1981 GAAGGGAGCGCGCGGGGACGGGAAACGGGACGAGGATAAGGACGACGAGAGAGAG 2040  
DB 1978 GACGAGAGCGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2031  
QY 2041 GACGGGACGAGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2100  
DB 2032 GGGGCGAGCGGGAGCGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2091  
QY 2101 GGGGCGCGGGTTCGCGACCCCACTTCGCGGTTTTCAGCTCGACCGCGCTGCTGTTTTCAC 2160  
DB 2092 GGGGCGAGGGTTCCTTGACCCCACTTCGCGGTTTTCAGCTGAAACCGCTGCTGTTTCGAC 2151  
QY 2161 TTTCGAGCTGTATCCCGAGCATATCCAGGCGCAACCTTGTGTTTTCAGTACGCTCTCC 2220  
DB 2152 TTTCGAGCTGTATCCCGAGCATATCCAGGCGCAACCTTGTGTTTTCAGTACGCTCTCC 2211  
QY 2221 CTGCGGCGGAGGCGGCTTCGCGACCTTCGAGGCGGAGCGGGAGCTACCTTGGAGTTCGAGGTG 2280  
DB 2212 CTGAGGCGGAGCGAGTGGGCGCACTTCGAGGCGGGAGGAGCTACCTTGGAGTTCGAGGTG 2271  
QY 2281 GGGGCGCGAGCGGCTGTTTTCGTAAGGCGCGACGTAAGCGAGAGCGCTTCGAGCATCTCTG 2340





Db	358	GGCGGCTTCTGGCCGCGCGCTTCGCGCTGTGGGCGCGGTGGACCAACGCCCCGCGGGG	417
Qy	421	TTGGAACCCACCGTACACCGTCTTCCACGTTGACACATCTCTGGAGCAGCTGGGAACACGCG	480
Db	418	TTCAACCCACCGTACACCGTCTTTCACGTTGATGACATCTCTGGAGAACGTTGGAGCACGCG	477
Qy	481	TACAGCATGCGGCGCGCCACGCTCAAGAGCGATTATGAGAGCCATCAGCCCGCGCGG	540
Db	478	TACGCGCATGCGCGCGGCCAGTTCCACGCGCGGTTATGGACGCGCATCACACGACGCGG	537
Qy	541	ACCGTCATCAGCTTCTGGGTCAGACCCCGGAAGCCATCGGTCGCGCGTTCAAGTCTAC	600
Db	538	ACCGTCATCAGCTCTTGGGCTGACTCCGGAAGGCCACCGGTTGGCCGTTTACGTTTAC	597
Qy	601	GGCACGCGGCAGTACTTTTATCATGAACAAGCGGAGGTGGATCGGCACCTCGCAGTGCCT	660
Db	598	GGCACGCGGCAGTACTTTTATCATGAACAAGGAGGAGTTGACAGGCACCTACATGCGCG	657
Qy	661	GCCCGCGCGATCTCTGCGAGGCGCTGGCGCGCCCTGCGCGAGTCCGCGGGGGGTG	720
Db	658	GCCCGCACGAGTCTCTGCGAGCGCATGCGCGCGCCCTGCGAGTCCCGGGCGCGTGC	717
Qy	721	TTCCGCGCATCTCGCGGACCATCTCGAGCGGAGGTGGAGCGGCGCGGAGTGTATC	780
Db	718	TTCCGCGGCACTCTCGCGGACCATCTCGAGCGGAGGTGGAGCGGCGCGAGTGTATC	777
Qy	781	TATTACGAACCGCGCCGACCCCTGTACTACGCGCTTCTGCTGCGAAGCGGCGCGCGCTG	840
Db	778	TACTACGAGACGCGCCCGCTCTGTGTTTACGCGCTCTACGTCGAGAGCGCGCGGTGCTG	837
Qy	841	GCCTACCTGTGCGCAAACTTTTGGCCCCCGCATGAGGAAGTACGAGGGGGCGTCGACGCC	900
Db	838	TCGTACCTGTGCGCAAACTTCTGCCCGCATCAAGAAGTACGAGGGTGGGGTCGACGCC	897
Qy	901	ACGACCCGGTTTATCTTGGACAAACCCGGGGTTTGTCACTTCGGCTGGTACCGCTCAAG	960
Db	898	ACCAACCCGGTTTATCTTGGACAAACCCGGGGTTGTCACTTCGGCTGGTACCGCTCAAA	957
Qy	961	CCGCGCGCGGGAACGCGCGGCCCAACCGCGCCCCCGACGGCGTTCGGAACCTCGAGC	1020
Db	958	CCGCGCGGGAACAACAACGCTAGCCAGCGCGGCCCCCGATGCGCTTCGGGACATCAGC	1017
Qy	1021	GACGTGAGTTTAACTGACGCGCGGAACAACCTGSCGCTCGAGGGGGCATGTGTGACCTG	1080
Db	1018	GATGTGAGTTTAACTGTAGCGCGGAACAACCTGGCCATCGAGGGGGCATGAGCGACCTA	1077
Qy	1081	CCGCGCTTACAAGCTCATGTGCTTCGATATCGAATGCAAGCGCGGGGGAGGACGAGCTG	1140
Db	1078	CCGCGCATACAAGCTCATGTGCTTCGATATCGAATGCAAGCGCGGGGGAGGACGAGCTG	1137
Qy	1141	GCTTTTCGGTTCGCGGAACGCCGGGAAGACTGTGCATCCAGATCTCCTCTCTGCTCTAC	1200
Db	1138	GCTTTTCGGTTCGCGGACCCCGGAGGACTGTGTATCCAGATATCCTGTCTGTCTCTAC	1197
Qy	1201	GACCTGTCCACCGCCCTCGAGCACATCTCCTGTTTTCGCTCGGATCCTCGGACCTC	1260
Db	1198	GACCTGTCCACCGCCCTCGAGCACATCTCCTGTTTTCGCTCGGATCCTCGGACCTC	1257
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Db	1258	CCCGAATCCCAACCTGAAACGAGCTGGCGGCGAGGGGCCCTGCCACGCGCGTGTCTGGAA	1317
Qy	1321	TTTTCACAGCGAATTTTCGAGATGCTCTGGCCCTTATGACCTTCGTTCAGCAGTACGGCCCC	1380
Db	1318	TTTCACAGCGAATTTTCGAGATGCTCTGGCCCTTATGACCTTCGTTCAGCAGTACGGCCCC	1377
Qy	1381	GAGTTTCGTGACCGGGTACAAACATCATCAACTTCGACTGGGCCCTTCGCTCTGACCAAGCTG	1440
Db	1378	GAGTTTCGTGACCGGGTACAAACATCATCAACTTCGACTGGGCCCTTCGCTCTGCGCAAGCTG	1437
Qy	1441	ACGAGATCTCAAGGTCCTCGCTCGACGGGTGAGGGCGCATGAACGCGCGGGGTGTCTTC	1500

Db	1438	ACGGACATTTACAAGGTCCTCCCTCGGACGGGGTA	CGCGCGCATGAACGGCGCGGGCGGTGTTT	1497
Qy	1501	CGCGTGTGGGACATCGGCGAGAGCCATTTT	CAGAAGCGCAAGATCAAGGTGAACCGGG	1560
Db	1498	CGCGTGTGGACATAGGCCAGAGCCA	CTTCCAGAGCGCAAGATAAAGGTGAACGGC	1557
Qy	1561	ATGGTGAACATCGACATGTACGGGATCAT	CACCGACAAGGTCAAACTCTCCAGCTCAAG	1620
Db	1558	ATGGTGAACATCGACATGTACGGGATTTA	TAAACCGACAAGATCAAGCTCTCGACTCAAG	1617
Qy	1621	CTGAACGCGCTGCGCGAGGCGCTCTTCA	AGGACAAGAAAGGATCTGAGCTACCGGAC	1680
Db	1618	CTAAACGCGTGGCGAAGCGCTCTG	AGGACAAGAAAGGACTTGAGCTATCGCGAC	1677
Qy	1681	ATCCCCGCTACTACGCTCTCGGCGCCG	CGCAGCGCGGGTGATCGGCGAGTATTGTGTG	1740
Db	1678	ATCCCCACTACTACGCGCGCGGCGCC	CGCAACGCGGGTGATCGGCGAGTACTGCATA	1737
Qy	1741	CAGGACTGCTGTGTGTGGGCACTGTTCTT	CAAGTTTCTGCGGCACTTGGAGCTTTTCC	1800
Db	1738	CAGGATTTCCCTGCTGTGTGGGCACTGTT	TTTAAAGTTTGTGCCCATCTCTGGAGCTCTCG	1797
Qy	1801	GCCTGCGGCGCTGTGGCGGCNTCAACAT	CACCGCGACCATCTACGACGCGCAGCAGATC	1860
Db	1798	GCCTGCGGCGCTGTGGCGGGTATTAA	CATCACCGCACCATCTACGACGCGCCAGCAGATC	1857
Qy	1861	CGCGTCTTACGTGCTCTGCGCGCTTGC	GGGGCCAGAAAGGCTTCATCTGCCGCGACACC	1920
Db	1858	CGCGTCTTACGTGCTGTGTGGGCGG	AGGCGCCCAAGGCTTCATCTGCCGCGACACC	1917
Qy	1921	CAGGGGCGGTTTGGGGCTCTGACAAG	AGGCGGCCCAAGCGCCGCTGCTCGGGGG	1980
Db	1918	CAGGGGCGATTTAGGGCGCGGGGGG	AGGCGCCCAAGGCTTCATCTGCCGCGACACC	1977
Qy	1981	GAAAGGAGCGCGCGGGGACGGGAG	CGAGGATTAAGACGACGACGAGGACGAG	2040
Db	1978	GACGAGAGCGCGCAGAGGAGGAG	GGGGAGCG-----AGAAACGACGCGAGGCGG	2031
Qy	2041	GACGGGACGAGCGCAGGAGGTGCGCG	CGAGACGGGGCGCGCACGTTGGGTACCAG	2100
Db	2032	GGGGCGAGCGGAGCGGAGGGCGCG	CGGAGACCGCGCGCACGTTGGGGTACCAG	2091
Qy	2101	GGGGCCCGGTCCTCGACCCCACTTCG	GGGTTTCAAGTCCGCCGCTGGTGGTTGAC	2160
Db	2092	GGGGCCAGGGTCCTTGACCCCACTTC	CGGTTTCAAGTCCGCCGCTGGTGGTTGAC	2151
Qy	2161	TTTTCGACCTGTACCCCGACATCATC	CAGGCCCAAACTGTGCTTCAAGCTCTCC	2220
Db	2152	TTTTCGACCTGTATCCCGACATCATC	CAGGCCCAAACTGTGCTTCAAGCTCTCC	2211
Qy	2221	CTGGGCGCGGAGCGCTGCGCGACCTG	GAGGCGGACCGGACCTCGAGATCGAGGTG	2280
Db	2212	CTGAGGGCGGACGAGTGGGCGCACTT	GAGGCGGAGGAGGACTACCTTGAGATCGAGGTG	2271
Qy	2281	GGGGCGCGACGGCTGTTTCTGTGA	AGGCGCCAGTACGCGAGAGCCTGCTGAGCATCTTG	2340
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Qy	2341	CTGCGGACCTGTGGCCATTCGAA	AGCAGATCCGCTCGCGGATTCGCCAGAGCACCCCC	2400
Db	2332	CTGGGGNACTGGCTCGCCATTCG	AAAGCAGATCCGCTCGCGGATTCGCCAGAGCACCCCC	2391
Qy	2401	GAGGAGGCGCTCTCTCGACAA	AGCAACAGGCGCCCATCAAGGTGTGTGCAACTCGGTG	2460
Db	2392	GAGGAGGCGGTCTCTCTGGA	CAAGCAGAGAGGCGCCCATCAAGGTGTGTGTA	2451
Qy	2461	TACGGGTTCACCGGGGCGCAG	CGGTCTTCTGCCCTGCTGCACTGTGCGGCCACCGTG	2520
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Qy	2521	ACGACCATATCGGCGCGCAG	ATGCTCTTCGCGACCGCGCGCTGACGTGCA	2580
Db	2512	ACGACCATATCGGCGCGCAGATG	CTGCTCGACCGCGGAGTACGTGCA	2571

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Db 2572 GCCTTCGACAGCTCCTCGCCGATTTCCGAGAGCGCGGCATGCGCGCCCCCGGCCC 2631
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Db 2632 TATTCATGCGCATCATCTACGGGACACGAGCTCCATATTTGTGCTGTGCGGGCCTC 2691
Qy 2701 ACGGCGCGCGCTGCTGCGCATGCGGCGAAGAATGGCGAGCCACATCTCGCGCGCGCTG 2760
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Qy 3061 CATCGCGCATCAACGACCGGAGAGGACATCCAGGACTTTGTCTTCCACCGCGAATG 3120
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RESULT 12
US-10-624-149A-1/c
; Sequence 1, Application US/10624149A
; Publication No. US20040109873A1
; GENERAL INFORMATION:
; APPLICANT: Neubauer, Antonie
; APPLICANT: Ziegler, Christina
; TITLE OF INVENTION: gm-Negative EHV-Mutants without Heterologous Elements
; FILE REFERENCE: 1/1372
; CURRENT APPLICATION NUMBER: US/10/624,149A
; PRIOR FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 60/403,282
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: DE 10233064
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: DE 10317008
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Version 3.0
; SEQ ID NO 1
; LENGTH: 150223
; TYPE: DNA
; ORGANISM: Equine herpesvirus 1
; PUBLICATION INFORMATION:
; AUTHORS: Telford, E.A.
; AUTHORS: Watson, M.S.
; AUTHORS: McBride, K.
; AUTHORS: Davison, A.J.
; TITLE: The DNA sequence of equine herpesvirus-1
; JOURNAL: Virology
; VOLUME: 189
; ISSUE: 1
; PAGES: 304-316
; DATE: JUL-1992
; DATABASE ACCESSION NUMBER: NC 001491, NCBI
; DATABASE ENTRY DATE: 2000-08-01
US-10-624-149A-1

Query Match 29,78; Score 1104.8; DB 19; Length 150223;
Best Local Similarity 59.13; Pred. No. 2e-271;
Matches 2131; Conservative 0; Mismatches 1317; Indels 156; Gaps 8;

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Qy 366 CTTCGCGCGCGTCTGCTTGGCGCTTGTGGGGCGGTGCGGACCATGCCCCCAAGGGGTTCGA 425
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Qy 546 CATCACGCTTCTGGGTCTGACCCCGAAGGCCATCGCGTTCGCGTTCACGTTCTAGGCAC 605
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QY 51846 CAACCTGTGTTTCCGACCTCGCGAAGACCCGACCTATGTTCCGGAATGACGTACC 51787
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3474 GCTCAACACGGAATTAATTTCTCGCACTGCTGGGGCGCGCTCGGTGAGCTTCAAGGC 3533
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 51786 GCTAAACACAGACTACTATTTCTCCACCTGTTGGGTACCATAAGCGTGAACCTTAAAGC 51727
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3534 CCTGTTTGGAAATAAGCCCAAGATCACCGAGAGTGTATAAGAGTTTATCCGAGAC 3593
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 51726 TCTATTCGGAATGATGTGAGAACACAGAAAAATCTTTTAAAGCGGTTTATTCGGAAC 51667
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3594 GTGGCAC---CCCCCGGACGCTGGCGCGCGGCTCAGGGCCGCGGGTTTCGGCGCGC 3650
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 51666 CCCCCAAGACCCCCACGAATAACCCAGGCACTGCTTGAGCGCGCCGCTTTGAAGCT 51607
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3651 GGGGCGCGCGCTACGCGGAGGAACCTGTCGAATGTTGCATAGAGCTTTGATACTCT 3710
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 51606 GACGCCCTTTTACCGCGGAGGAAGAAAGTGTGCGAATACTGCAATACAGTCTTGTACTCT 51547
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3711 AGCA 3714
Db |||||
QY 51546 AGAA 51543
Db |||||
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RESULT 13
US-10-626-832-155
; Sequence 155, Application US/10626832
; Publication No. US20050003342A1
; GENERAL INFORMATION:
; APPLICANT: Davis Poynter, Nick
; APPLICANT: Nugent, Josephine
; APPLICANT: Birch-Machin, Ian
; APPLICANT: Allen, George P
; TITLE OF INVENTION: Viral Marker
; FILE REFERENCE: 620-262
; CURRENT APPLICATION NUMBER: US/10/626.832
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/398,576
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 155
; LENGTH: 3663
; TYPE: DNA
; ORGANISM: Equine herpesvirus 1
US-10-626-832-155

Query Match      29.6%; Score 1100; DB 21; Length 3663;
Best Local Similarity 59.0%; Pred. No. 2e-270;
Matches 2128; Conservative 0; Mismatches 1320; Indels 156; Gaps 8;

QY 186 GGTTCAGCGGCATACGTACTACGAGTGGCGAGAAATTTGATTTATCGCCCGCGTTC 245
Db 120 GCGCCCGCAACACTCGTACTGCACAGAGTGGGTAGCTTTAAAGTTTATAGTCTCAAGATG 179

QY 246 GCTGGAGAGGACGCCCGCGGAGCAGCACCGGGTCCACGCGCGCCCTCCGCGC 305
Db 180 CCTCGATGAAGAACCCCGCGACGAGCGGCTGACACGTGGGCACCTTGGAGCG 239

QY 306 CGCCCTTAAGGTGTACTCGCGGGGAGCAGCGCGAGTCTCTCGCGTGGCGCGGAGGG 365
Db 240 CCACCCAAAGTGTACTGCGATGGCTCAGAGTACGACGTCTGAACTTTGGCTCGGAGG 299

QY 366 CTTTCGCGCGGTGCTGCGGCGCTTGGCGGCGGTGGCGACCATGCCCCCAAGGGTTCGA 425
Db 300 TTGTCGCGCTCGAGGATTCGGGTTTGAACCGGCAGGATTTTCGGGCGATGGAATTCGA 359

QY 426 CCCCACCGTCACTGCTTCCACGTGTACGATCCTCGAGCAGCTGGAACACGCGTACAG 485
Db 360 CCCAGATTTAGAGATTTTACGTGTACGATAGTAGAGACTTCGGAGAGCGCTTACA 419

QY 486 CATCGCGCGCCCGCAGCTCCACGAGCGATTTATGGACGCCATCACGCCCGCGCGGACCGT 545
Db 420 CGATGACCCATCCAGGTTTGTGAGCTAT-----CCGCGCCCAAGCGGTCTGT 467

QY 546 CATCAGCGTTCGGGTCTGAGCCCCCGAAGGCCATCGCGTTCGCGGTTCAGTCTACGGAC 605
Db 468 GGTAAACACTGCTGGGAATGAGCGAGTGTGGAACGAGTTCGCGGTTCACGCTTATGGTGT 527

QY 606 GCGCGAGTACTTTTACATGAACAGGCGAGTGTGATCG----- 644
Db 528 GCGCCATTAATTTTACATGGCAAGCGGAGGTGATAGCCCTTGTGGAATAACACCGCA 587

QY 645 -----GCACCTCGAGTGCCTGCCCGCGC-----GATCTCT 676
Db 588 GGCAGAACTCGTGCAGCAATGGTGGACTGCGCGCACAGCTCGGCTTTGAGCGCGGCTCT 647

QY 677 GCGAGCGCTTGGCGCGCGCCCTGCGGAGTCCCGGGGCGTTCGTCGCGG----- 728
Db 648 GGGAAATGGCAACCGCGCAACACAGAGCGCGGAGCGCGGGGGAATGGTGGGCGGAAA 707

QY 729 ---CATCTCCGCGACCACTTCGAGGCGGAGTGTGGAGCGCGCGACGTGTACTATTA 785
Db 708 GCACGTGTCTGGGACTGCTTCAAAGTGGAGACCGTGTGCGCACAGACGCTGTACTATT 767

QY 786 CGAAACGCGCCGACCTCTGTACTACCGGCTTTCGTGCGAAGCGGCGCGCTGGCCCTA 845
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Db 768 TGGATCTAAGCCAGCTCTCTCTATATAGATATCTGCTCCAGCAGCGCTCGGGGGT 827  
Qy 846 CTTGTGCGCAAACTTTTGGCCCGGATCAGGAAGTACGAGGGGGGCTCGACCCACCAC 905  
Db 828 CATCTGGGCACTTTTACCCCGAGATTACAAATTCGAGGGAGGCTGGACGTACCCAC 887  
Qy 906 CCGGTTTATCTTGGCAAAACCCGGGGTTTGTACCTTTGGCTGTGTACCGCTCAAGCCCGG 965  
Db 888 CGGGCTGTGTGGCAAAATGAAAAATTTTACCAAGTTTGGGTGTACCGCTCGGACCCGG 947  
Qy 966 CCGGGGAACGCGCGGCCCAACCGGCCCGGACCGGGTTCGGAACTTCAGGACGT 1025  
Db 948 CACCACGAGAGCGTGTTCAACTTCGCCCCGTTGAGCGACGCTCACTCAAGCGAGCT 1007  
Qy 1026 CCGATTTAACTCGACGGCGGCAACCTGGCCGTCGAGGGGGCATGTGTGACCTCGCCGC 1085  
Db 1008 GAGATTAATCTGTACTCCCGATAACCTGGAGCCGATACAGAGGAGCTGCTGGCCGA 1067  
Qy 1086 CTACAAGCTCATGTCTTCGATATCGAATGCAAGGCGGGGGGAGGACGAGCTGGCCCT 1145  
Db 1068 CTATAAGCTCATGTCTTGTATATAGATGTAAAGCTGGAACTGGAATGCGGT 1127  
Qy 1146 TCGGTCGGGAACCGCCCGGAAGACTTGTATTCAGATCTCTGTCTGTCTAGACT 1205  
Db 1128 CCCAGTGGCAACTAACCAGAGAGGACTTGGTCATCCAGATCTCTGTCTGTCTAGCT 1187  
Qy 1206 GTCCACACCGCTCGAGCACATCTCTGTCTTTCGCTCGGATCTCTGACCTCCCGA 1265  
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Qy 1326 CAGCGAATTCGAGATGCTGCTGCTTCTATGACCTTGTCAAGCAGTAGCGGCCCGAGTT 1385  
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Qy 1386 CQTGACCGGTACAACATCATCACTTCGACTGGCCCTTCGCTGACCAAGCTCAGCGA 1445  
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Qy 1446 GATCTACAAGGTCCCGCTCGACGGGTACGGGCGCATGAACGGCGGGGTGTTCGGGT 1505  
Db 1428 GGTGTATAACATCAAGCTTGAAGCTAGCGGTACGCAAGTTCAACAAGGGGGCTGTAAAGT 1487  
Qy 1506 GTGGACATCGCCGAGAGCACTTTTCAGAAAGCGCAGCAAGATCAAGGTGAACGGAGTGT 1565  
Db 1488 GTGGACATCGCCACGAACCAATTTTCAGAAAGAGCAAGGTGAATAATCAATGGGCTGAT 1547  
Qy 1566 GAAACATGACATGTACGGCATCATCAACGACAAGGTCAAACTCTCCAGCTACAAGCTGA 1625  
Db 1548 ATCTCTAGACATGTATTTCTGTGGCAGCGAAAGCTTAAGCTTACCAGCTACAAGCTGA 1607  
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Db 1608 CGCGCTCGTGGAGAGCTCTCGCGAGCATTAAGATAGACCTTCCCTATAAAGAAATACC 1667  
Qy 1686 CGCCTACTACGCTCGGGCCCGCGAGCGGGGTGATCGCGCAGTATTTGTGTCCAGGA 1745  
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Qy 1746 CTGCTGTGTGTGGGAGCTGTCTTCAAGTTTCTGCGCACTGGAGCTTTCGCCGT 1805  
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Qy 1806 CGCGCTCGGGGCGCATCAACATCACCCGCAACCTCTACGACGGCCAGCAGATCCGGT 1865  
Db 1788 GGCACAACTCGCCGTATCACCTTAACCGGGTAAATTTTGACGGTCAGCAAAATTCGGT 1847  
Qy 1866 CTTACGTGCTCTCGCGCTTGGGGCGAGAGGGCTTTCATCTCGCGGACACCCAGGG 1925  
Db 1848 GTACACGTGTGCTGAAACTCGCCCGGAGAGAAATTTTCAATTTTGGCAGACAAACAGACG 1907

Qy 1926 GCGGTTTCGGGGCTCGACAAGAGGAGCGCCCAAGCGCCCGGCGCTGCTCGG----- 1978  
Db 1908 CCGGTTTGAAGTACAGGACAGACCGCGCTCAGAGACTTCGGAGTTGGCTATGATAGCCA 1967  
Qy 1979 -----GGAAAGGGAGCGCGCGGGGACGGGAAACGGGACGAGGATAGAGACGACAGCA 2033  
Db 1968 AAGCCACGCTTCGACAGTACAGACGAACCCGACGGTGTGACGGTACCCCGAGCGCGC 2027  
Qy 2034 GGAACGAGGAGGAGCGCGGAGGAGGTTCGCGCGCAGACCGGGGGCGGCGACGTTGG 2093  
Db 2028 AGGATCTGGCGCTACTTCTGAAAAACGAGGCGGGAAGCCCGCTCGGGAGGGCGGTGG 2087  
Qy 2094 GTACAGGGGGCGGGGCTCTCGACCCCACTCCGGTTTACGCTCGACCGCCGTGTGT 2153  
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Qy 2214 GCTCTCTCGGGCGGAGGCGCTCGGACCTGAGAGGGGACCGGGACTACTCTGAGAT 2273  
Db 2208 CTTGGCGCTCGATGAAGTGGATCTGGCCGGGCTTCAACCATCCGTCAACTACTCTGACGTT 2267  
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Qy 2634 CGGTCGCTTCCATGCGCATCATCTACGGGACACGAGTCCATTTTGTGTTTGTGCGCG 2693  
Db 2628 CAAGCTTACTCTCGTCAGGGTTATCTACGGAGACACCGACTCCGTGTTTATCAAGTTGT 2687  
Qy 2694 CGGCTCAGCGCGCGGGCTGTGGCCATGGGCGCAAGATGGGAGCAGACATCTCGCG 2753  
Db 2688 GGGCTGAGCTACGAGGGGTATCGGAGCTGGGGATGCTATGTGCGGTGAGATTTTCAAG 2747  
Qy 2754 CGGCTGTCTCTCCCCCGATCAAGCTGAGTGGAAAAAGTTTCAACAGCTGCTGCT 2813  
Db 2748 GGACCTCTTATAGCGCCCATCAAACTGGAGTGTGAGAAAGCCTTTTTCAGCGACTGCTGCT 2807  
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Db 2808 GATCAACCAAGAAAGTACATAGGTGTCTAAACGGGGGGAAGATGCTCATGAAAGGGGT 2867  
Qy 2874 GGATCTGTGCGCAAAAACAACTGCGGCTTTATCAACCGCACTCTCAGGGCCCTGCTGCA 2933  
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Qy 2934 CTTGCTGTTTACGACGATACGTTATCCGAGCGGCGCCCGGCTTGTAGCGGAGCGCCCGC 2993  
Db 2928 TCTTTTGTGTACGACGAGGATGTGGCCACCGCGCGCAGCAAAAGGTGACAGACGCTGCCCTCC 2987







QY 3294 GCTAGACGCCGCCGCCAGGGAGAGCGCGCCGCCCGCCCGCCCTGCCCTCCCGGC 3353  
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QY 3354 CAAGCGCCCGCGGAGAGCGCGTGCATGCCGACCCCGCGGAGCGCGTCCAAGCCCGC 3413  
Db 51798 ACGCCCCCAACTAA-----ACG 51781  
QY 3414 CAAGCTGTGTGTTCGAGTGGCGGAGGATCCCGGGTAGCGCATCGCCCGGGGGGTTC 3473  
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QY 3474 GCTCAACAGGACTATTACTTCTGCACCTGTGGGGCGCGCTCGGTGAGAGTTCAGGC 3533  
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QY 3651 GGGGCGCGGCTACCGCGGAGGAAACTCGTCGATGTTGCATAGAGCCTTTGATACTCT 3710  
Db 51540 GACGCGCTTTACACGGGAGGAAGTCTGCGAATATGTCATACAGTTTTTTGTACTCT 51481  
QY 3711 AGCA 3714  
Db 51480 AGAA 51477

## RESULT 15

US-10-624-149A-2/c  
; Sequence 2, Application US/10624149A  
; Publication No. US20040109873A1  
; GENERAL INFORMATION:  
; APPLICANT: Neubauer, Antonie  
; APPLICANT: Ziegler, Christina  
; TITLE OF INVENTION: GM-Negative EHV-Mutants without Heterologous Elements  
; FILE REFERENCE: 1/1372  
; CURRENT APPLICATION NUMBER: US/10/624,149A  
; PRIORITY FILING DATE: 2003-07-21  
; PRIOR APPLICATION NUMBER: 60/403,282  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: DE 10233064  
; PRIOR FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: DE 10317008  
; PRIOR FILING DATE: 2003-04-11  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent In Version 3.0  
; SEQ ID NO 2  
; LENGTH: 145597  
; TYPE: DNA  
; ORGANISM: Equine herpesvirus 4  
; PUBLICATION INFORMATION:  
; AUTHORS: Telford, E.A.  
; AUTHORS: Watson, M.S.  
; AUTHORS: Perry, J.  
; AUTHORS: Cullinan, A.A.  
; AUTHORS: Davison, A.J.  
; TITLE: The DNA sequence of equine herpesvirus-4  
; JOURNAL: J. Gen. Virol.  
; VOLUME: 79  
; ISSUE: 5  
; PAGES: 1197-1203  
; DATE: MAY-1998  
; DATABASE ACCESSION NUMBER: NC 001844, NCBI  
; DATABASE ENTRY DATE: 2000-08-01  
US-10-624-149A-2

Query Match

23.8%; Score 885.8; DB 19; Length 145597;

Beet Local Similarity 55.2%; Pred. No. 1.5e-215;  
Matches 1986; Conservative 0; Mismatches 1452; Indels 159; Gaps 7;  
QY 193 CGCATAGTACTACTAGCGAGTGCAGCAATTTTCGATTTATCGCCCGCGCTTCGTGAC 252  
Db 54795 CACCACCTACTACTACCGAGGTGGCAACTTCAAGTTTCATAGCACCAAGTCTTGTAT 54736  
QY 253 GAGACGCCCGCGGAGAGCGCACCGGGGTTCACGACGGCCGCTCCGGGGCGCCCT 312  
Db 54735 GAAGATGCTCAACCGATCAGCGACGCGTGTGATGTGGGAAACACTTGAAGCGCACCCCA 54676  
QY 313 AAGGTGTACTCGCGGGGAGACGAGCGCACTCTCCGCGTGGCGCCGAGAGGGCTTCGG 372  
Db 54675 AAGGTGTACTGTGATGGCGAGATACGACGTCTTAGCTTTGAAGTGAAGTGTCTGG 54616  
QY 373 CCGCGTCCGTTGCGCTGTGGGGCGGTGCGGACCATGCCCCAAAGGGGTTTCGACCCAC 432  
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QY 433 GTACCGCTCTTCCAGGTGTACGACATCTTGAGACAGCTGGAAACACGCGTACAGCATGCGC 492  
Db 54555 TTTGAGAGGTTTCAGCTGTACGACATAGTAGTGTGGAAAGCGCTTCGAAACGACGAC 54496  
QY 493 GCGCCCGAGCTCCACGAGCGATTTATGAGCCCATCAGCCCGCGGACCGTCATCAGC 552  
Db 54495 CCGTCGCGGTTTGTGAGCTATCT-----CGCCCAAGCGGATCAGTGGTAAACA 54448  
QY 553 CTTCTGGGTCTGACCCCGAGGCCATCGCGTCCCGTTACGTTACGGCACCGGCGAG 612  
Db 54447 TTGCTGGGAATGAGCGAATGTGGAAAGCGCGTAGCGGTTACGTTGACGGTGTGCGCCT 54388  
QY 613 TACTTTTACATGAACAAGCGGAGTGGATCG-CCACTGCAAGTCCGTGCCCGCGCA 671  
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QY 672 TCTCTGAGCGCGCTGCGCGCGCCCTCGCGAGTCGCGGGGGCGCTGTTCCCGCGCAT 731  
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QY 732 CTCCGCGACACATTCGAGGCGGAGGTGGTGGAGCGCGCGCAAG-----775  
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QY 853 GACAACTTTTCCCGCGATCAGGAATGACGAGGGGGCGTTCGACGCCACACCGCGTTT 912  
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QY 913 ATCTGGACACCGCGGGTTGTCACTTCGGCTGGTACCGCTCAAGCCCGCGCGGG 972  
Db 54027 TTGTTGACAAATGAAAATTTTACAGTTTGGTGGTACCGCCCTCGCGCCGGAACCAAC 53968  
QY 973 AACGCGCGGCGCAACCGCGCCCGCGCGTTCGGAACCTTCGAGCGAGCGTTCGAGTTT 1032  
Db 53967 GGAGAGCGTGTCAACTGCGCCAGGTAGAGCGACACCTGACCTCAAGTACGTTGAAAT 53908  
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QY 1153 GCGGAACCGCGGAGACCTCGTCATCCAGATCTCTGTCTGTCTTACGACCTGTCCACC 1212



53787 GCACTAAACAAGAGACTGGTAATTCAAATTTCTGTTGCTTTACTCTTTTAGCAACC 53728  
1213 ACGCCCTCGAGACATCTCTGTTTTCGCTCGATCTCGACCTCCCGAGTCCCAAC 1272  
53727 CAAAGCATGAACACACCTCTGTTTCTTAGGTCTGTGATATTTCTGAAGATAC 53668  
1273 CTCAGCGATCTCGCTCCAGGGCCCTGCGGCCCGCTGCTCTCGAGTTTTCAGACGAA 1332  
53667 GCTTCTGGCTGTGTACAACGCGGGGAACTAGCCCAACAGCTCTTGGAGTTTATAGCGAA 53608  
1333 TTGAGATCTGCTGCTCTCATGACCTTCGTCAGCAGTACGGCCCGAGTTCTGTACC 1392  
53607 TATGAGCTGTGATAGCATTTTAAACATTTCTCAAGCAATCTCTCCAGAGTTTCCACT 53548  
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53547 GGTACAACTTTGTAACCTTTCGCTGGGGGTACATAGTTTAAAGTTTACGCTCCGTTAT 53488  
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53487 AACATAAACTTGTATGGGTACGGCAAGTTTAAACAAAGGAGGCTGTTTAAAGTCTGGAC 53428  
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53127 CTAGCCCGATAACTTAAGCGGGTAAATTTTGTGTCAGCAAAATTCGCGTTTACACA 53068  
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1933 CGGGGCTCGACAGGAGCGCCCAAGCGCGCGCTGCTCGGGGGAGGGAGCGG 1992  
53007 GACTACCATGGGAGCTGTGTGGAAAGTTCCGAGACATCATATAATAGTGAAGACCAC 52948  
1993 CGGGGGAGCGGAAACGGGGAGCGAGTAA-----GGAACGACGAGGAGGAGCG 2044  
52947 GCTTTGACAAACAATAACAATCAGATAGTATTAATGGAGCCAGATGTTATAGTCTG 52888  
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52887 TCTGCAATTTTGGAAACAGGGGGCGGAAACCCGGCACAGGTAGGATTTGTGGATACCAA 52828  
2101 GGGGCGCGGCTCTCGACCCACCTTCGCGTTTACGTCGACCCCGTGTGTGTGTTTTCAC 2160  
52827 GGAGCAAGGTGTAGATCTTATCTCGCTTTCATGTTGACCCAGTGTGTGTGTTGAC 52768  
2161 TTGCGAGCTGTATCCCGACATCATCCAGGCCCAACACCTGTGTCTCAGTACGCTCTCC 2220  
52767 TTGCGAGCTGTATCCCGACATCATCCAGGCCCAACACCTTTGTTTCCACACCTTAGCC 52708  
2221 CTGCGGCGGAGCGCTCGGACCTCGAGGGGACCGGACCTACCTGGAGATCGAGGTG 2280  
52707 CTTAATGAAGTGGATTTGGCTTTCAGCGGCTTTCAGCGGTGTGTGACTACTCAACGTTTGAGGTG 52648

2281 GGGGCGCGAGCGCTGTTCTTCTGTAAGGCCACGTACGAGAGCTGCTGAGCATCTCG 2340  
52647 GCGGACCAAAAGTTGTTTGTGTCAGCGGCACATTCGGGAAGCTTGTCTGTTATTTG 52588  
2341 CTGCGGATCGCTCGCCATCGAAAGCAGATCCGCTCGCGATCCCGCAGACACCC 2400  
52587 CTGCGGATCGCTCGCTATCGAAAGCTGTAGGGCAGAAATTCACAAAGTACCCG 52528  
2401 GAGGAGCGCTCTCTCGACNAGCAACAGGCGGCATCAAGTGTGTGTCACCTCGGTG 2460  
52527 GAGGAGCGAGTTTCTAGATAAGCAACAGTCTGCAATTAAGTAATATGCAACTCAGTT 52468  
2461 TACGGTTTCAACGGGCGCAGCAGCTCTTCTGCGCTGCTGCACTGTCGCGCCGACCGGTG 2520  
52467 TACGATTTACCGGTGTGGCAACCGACTGTTGCCATGCTCTGAGATAGCAGCCGTT 52408  
2521 ACGACATCGCGCGGAGATGCTCTCGCAGCGCGGTACGTGACGCGCTGGCG 2580  
52407 ACTACATAGGCGGCAACATGCTTCTCAAAACGAGAGATTACGTTCACTATCGTTGGCG 52348  
2581 GAGTTGATCAGCTGCTGGCGCAGCTTTCCGAGGCGCGGATCGCGCCCGCGCTCG 2640  
52347 ACGCTGAGCTGTTGGAAACAACTTCCAGGGGCTTTAAATTTTCGCAACCAACGCT 52288  
2641 TACTCCATCGCATCATCTACGGGACACGGAATCTCAATTTCTGTTTGTGCGCGGCTC 2700  
52287 TATCTGTGAGTTTATTCGAGACACCGACTCTGTATTCATCAAGTTTGTGGCTA 52228  
2701 ACGCGCGCGGCTGTTGCGCATGCGGCAAGATGGCGAGCACATCTCGCGCGCTG 2760  
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2761 TTCTCTCCCGCATCAAGCTCGAGTGCAGAAAGGTTTCAACAGCTGCTGCTCATCGC 2820  
52167 TTTAAGCACCTATCAAACTAGAGTGTGAAGAAACCTTCCAGCGGCTGCTACTAATACA 52108  
2821 AAGAAAAAGTACATCGCGCTCATCTCGGGGCAAGATGCTCATCAAGCGCTGATCTG 2880  
52107 AAGAAAAAGTACATAGTGTATCAACGGGGGTATATGCTCATGAGGGGTAGACCTA 52048  
2881 GTGCGCAAAAACTGCGCTTTATCAACCGCACCTCCAGGGCTCTGTCGACCTGCTG 2940  
52047 GTCGTAAAAATACTGTGCTTATATAAATCTTACGCGGACATCTAGTAGATCTTCTG 51988  
2941 TTTTACGACGATACTGTTACGAGCGCGCGCTTACGCGAGCGCCCGCAGAGGAG 3000  
51987 TTGTACGAGGAGGAGTACTACCGCGCGCGGAGGTAACTAACGCTGCTCTCCACAG 51928  
3001 TGGCTGCGCGACCTCTCGCGAGGAGTCAAGGCTTTCGCGCGCTCTCTGAGACGCG 3060  
51927 TGGTTGGCGCGCTTCCGAGCGCTTTCAGAGTTTGGAGAGTGTGATAGAGCT 51868  
3061 CATCGCGCATCAACGAGCGGAGGAGCATCCAGGACTTTGTCTTCCACCGCGAAGCTG 3120  
51867 TACAACGTAATAACGACCCCACTTGGATGTGCGGAGTTTGTGATGACGCTGAGCTT 51808  
3121 AGCAGACACCGCGCGGTACACCAAGCGCTTGGCCCACTGACCGGTGTATTACAG 3180  
51807 AGCCGACCGCGGAATCATATACAAAGCGGCTTACCGCACTCTGTTTACTTTAAG 51748  
3181 CTCTGCGCGCGCGCGCTCTCCGCTCATCAAGGACCGGATCCCGTACGCTGATCTG 3240  
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3241 GCCCAGACCGCGAGGTAGAGGAGACGCTCGCGGGTGGCGGCTCTCCGAGGCTAGAC 3300  
51687 GCGCAACAGAAAGCGCTGAACGCGAAGCTTGTATAGTAAACTCCATCGCTG----- 51636  
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51635 ----- 51636

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Qy 3361 CCCGGGAGACCGCTCGCATGCCGACCCCGGGAGCGGTCCAAGCCCGCAAGCTG 3420
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Qy 3421 CTGGTGTCCGAGCTGGCGAGGATCCCGGGTACGCCATCGCCCGGGCGTTCCGCTCAAC 3480
Db 51579 CTCGTTCCGACCTGGCTGAGGATCCACCTATGTTTCAGAAAATGAGGTTCCACTTAAC 51520
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Db 51519 ACAGACTACTATTTTTCCACCTGTGGGTACGATAAGCGTAACCTTTAAGGCATTATTT 51460
Qy 3541 GGAATAACGCCAAGATCACCGAGTCTGTTAAAGGTTTATTCCCGAGACGTGGCAC 3600
Db 51459 GGAAATGATGCAAAAGACCACAGAAAACCTTTTAAAGCGATTATTTCAGAAAAGACCCAC 51400
Qy 3601 ---CCCCCGGACGCTGGCGCGCGCTCAGGGCCGCGGGTTTCGGGCCCGCGGGGCC 3657
Db 51399 AAGACCTCCACAAAACCCAGGAGATGTTGGAGCGCGCTGGATTGAAAAGCTAACTCCC 51340
Qy 3658 GCGGCTACGCGGAGGAAACTCGTCGAATGTTGCATAGAGCCTTTGATCTCTAGCA 3714
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Job time : 2235 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 5, 2005, 23:52:49 ; Search time 1860 Seconds

(without alignments)  
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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001as.\*
- 5: Geneseq2001bs.\*
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- 8: Geneseq2003as.\*
- 9: Geneseq2003bs.\*
- 10: Geneseq2003cs.\*
- 11: Geneseq2003ds.\*
- 12: Geneseq2004as.\*
- 13: Geneseq2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3717	100.0	3717	6	AAD30077 Herpes si
2	3696.2	99.4	3723	6	AAD30078 Herpes si
3	3696.2	99.4	14926	2	AAD30078 HSV-2 str
4	3696.2	99.4	117213	2	AAD30078 HSV-2 str
5	3693	99.4	154746	6	AAD30078 Human her
6	3059.8	82.3	3708	6	AAD30079 Herpes si
7	3053.4	82.1	3708	6	AAD30080 Herpes si
8	3047	82.0	3708	6	AAD30081 Herpes si
9	1104.8	29.7	149158	12	ADP74211 Equine he
10	1104.8	29.7	149261	12	ADP74212 Equine he
11	1104.8	29.7	150071	12	ADP74216 Equine he
12	1104.8	29.7	150223	12	ADP74201 Equine he
13	1100	29.6	3663	12	ADJ95524 Equine he
14	885.8	23.8	144411	12	ADP74214 Equine he
15	885.8	23.8	144486	12	ADP74215 Equine he
16	885.8	23.8	145444	12	ADP74213 Equine he
17	885.8	23.8	145596	12	ADP74202 Equine he
18	701.8	18.9	124884	5	AAD30081 Nucleotid
19	701.8	18.9	124884	10	ADP74201 Human her
20	701.8	18.9	124884	11	ADL99489 Varicella

c	21	697	18.8	125157	5	AAH74202
	22	517.2	13.9	554	12	ADP82907
	23	515.4	13.9	558	12	ADP82906
	24	319.4	8.6	3048	2	AAH60714
c	25	319.4	8.6	172281	12	ADN12161
	26	313.2	8.4	128139	6	AAI64291
	27	313.2	8.4	133719	3	AAH64754
	28	243.6	6.6	2511	2	AAH51553
	29	242	6.5	35100	2	AAV73802
	30	242	6.5	137507	2	AAV19941
	31	242	6.5	137508	12	ADN12162
	32	219	5.9	231	13	ADK51364
	33	191.2	5.1	228	2	AAQ13715
	34	187	5.0	231	13	ADK51363
	35	169.2	4.6	3729	6	AAH30082
	36	164.4	4.4	3729	13	ADR19896
c	37	164.4	4.4	229354	6	ABQ74179
	38	153.2	4.1	3039	2	AAQ91096
	39	130	3.5	536	2	AAH51545
	40	110.6	3.0	536	2	AAH51546
	41	101.4	2.7	103	2	AAH31980
	42	90.2	2.4	103	2	AAH31979
	43	89	2.4	454	2	AAH51554
	44	89	2.4	3435	2	AAH35869
	45	89	2.4	3443	5	AAH79309

#### ALIGNMENTS

##### RESULT 1

AAD30077

ID AAD30077 standard; DNA; 3717 BP.

XX AAD30077;

XX AAD30077;

DT 17-MAY-2002 (first entry)

DE Herpes simplex virus (HSV2-MS-M1) mutant DNA polymerase gene.

XX Herpes virus; medicinal; therapy; binding domain; DNA polymerase gene;  
KW antiviral; enzyme; mutant; ds.

XX Herpes simplex virus.

XX Key Location/Qualifiers

FT CDS 1..3717

FT /\*tag= a

FT /product= "Mutant DNA polymerase"

XX WO200206513-A2.

XX 24-JAN-2002.

XX 13-JUL-2001; 2001WO-US016525.

XX 13-JUL-2000; 2000US-0218118P.

XX 13-APR-2001; 2001US-0283880P.

XX (PHAA ) PHARMACIA & UPJOHN CO.

XX Homa FL, Wathen MW, Hopkins TA, Thomsen DR;

XX WPI; 2002-179800/23.

XX P-PSDB; AAE18853.

PT Selecting compounds that inhibit herpes viruses by comparing inhibitory  
concentration of a compound of interest that inhibits wild-type herpes  
virus and domain mutant herpes virus, and selecting compound of interest.

XX Claim 25; Fig 5; 126pp; English.

XX The present invention relates to a method for selecting compounds that

CC inhibit herpes viruses. The method involves measuring IC 5.0 of compound  
CC of interest that inhibits wild-type herpes virus and domain mutant herpes  
CC virus mutant herpes virus which is the same strain as wild-type herpes  
CC virus, comparing IC 5.0 of the compound inhibiting wild-type herpes virus  
CC with IC 5.0 of the compound inhibiting mutant herpes virus and selecting  
CC the compound, where IC 5.0 of the compound of interest that inhibits  
CC mutant herpes virus is at least 3 times greater than IC 5.0 of the  
CC compound that inhibits wild-type herpes virus. The method is useful for  
CC selecting compounds that inhibit herpes viruses. The compound is useful  
CC for manufacture of medicinals for selectively treating diseases caused by  
CC herpes viruses such as herpes viral infection, or for selectively  
CC inhibiting herpes viruses, in a human host by administering a compound to  
CC human in need of such treatment, where the compound inhibits herpes  
CC viruses by interaction with the binding domain in the viral DNA  
CC polymerase, and IC 5.0 of the compound that inhibits a binding domain  
CC mutant herpes virus is at least 3 times, preferably 5 times greater than  
CC IC 5.0 of the compound that inhibits the wild-type herpes virus which is  
CC the same strain as the mutant herpes virus. The present sequence is  
CC Herpes simplex virus (HSV2-MS-M1) mutant DNA polymerase gene  
XX  
SQ Sequence 3717 BP; 627 A; 1293 C; 1200 G; 597 T; 0 U; 0 Other;

Query Match 100.0%; Score 3717; DB 6; Length 3717;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3717; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGTTTGTGCGGGGCGCGCGACTTCCCGGGGGGAAGTCGGGGCTCGGGCGGG	60
Db	1	ATGTTTGTGCGGGGCGCGCGACTTCCCGGGGGGAAGTCGGGGCTCGGGCGGG	60
Qy	61	TCGTGGGTTTTTGGCCCCCAACACCCCGGGGAGCCACCCAGACGGCAGCCGCGCTTC	120
Db	61	TCGTGGGTTTTTGGCCCCCAACACCCCGGGGAGCCACCCAGACGGCAGCCGCGCTTC	120
Qy	121	CGCGCGCAGAACTTCTACACCCCGCTCGCTAGACCGGAAACGCAAGGCCCC	180
Db	121	CGCGCGCAGAACTTCTACACCCCGCTCGCTAGACCGGAAACGCAAGGCCCC	180
Qy	181	GGGCGGCTCAGCGGCATAGTACTACGAGGAGTCGACGAAATTCGATTTATCGCCCG	240
Db	181	GGGCGGCTCAGCGGCATAGTACTACGAGGAGTCGACGAAATTCGATTTATCGCCCG	240
Qy	241	CGTTTCGTGACGAGAGCGCCCGCGAGCAGCGCACCGGGTCCACGACGGCGGCTC	300
Db	241	CGTTTCGTGACGAGAGCGCCCGCGAGCAGCGCACCGGGTCCACGACGGCGGCTC	300
Qy	301	CGCGCGCCCTAAGGTGTACTGCGGGGGGACGAGCGGACGTCCTCCGCTGGGCGG	360
Db	301	CGCGCGCCCTAAGGTGTACTGCGGGGGGACGAGCGGACGTCCTCCGCTGGGCGG	360
Qy	361	GAGGGCTTCTGGCGCTGCGCTTGGCGGTGGGGCGGTGGGACCATGCCCCMAGGG	420
Db	361	GAGGGCTTCTGGCGCTGCGCTTGGCGGTGGGGCGGTGGGACCATGCCCCMAGGG	420
Qy	421	TTGACCCCGCTCAGCGTCTCCAGGTGTACGACATCTCGGAGCAGCTGGAAACGCG	480
Db	421	TTGACCCCGCTCAGCGTCTCCAGGTGTACGACATCTCGGAGCAGCTGGAAACGCG	480
Qy	481	TACAGCATGCGCGCCGCGCAGTCCACGAGCATTTATGACGCGCATCAGCCCGCGGG	540
Db	481	TACAGCATGCGCGCCGCGCAGTCCACGAGCATTTATGACGCGCATCAGCCCGCGGG	540
Qy	541	ACCGTCATCAGCTTCTGGGTCTGACCCCGGAAGGCGCATCGCTCGCGGTTCAGTCTAC	600
Db	541	ACCGTCATCAGCTTCTGGGTCTGACCCCGGAAGGCGCATCGCTCGCGGTTCAGTCTAC	600
Qy	601	GGCAGCGGCGAGTACTTTTATCAACAAAGCGGAGGTGGATCGGCACCTGCGAGTCCGT	660
Db	601	GGCAGCGGCGAGTACTTTTATCAACAAAGCGGAGGTGGATCGGCACCTGCGAGTCCGT	660
Qy	661	GCCCCGCGCATCTCTCGAGCGCTTGGCGCGCCCTTGGCGAGTGGCGGGGGCGTGG	720
Db	661	GCCCCGCGCATCTCTCGAGCGCTTGGCGCGCCCTTGGCGAGTGGCGGGGGCGTGG	720

Qy	721	TTCCGCGGCATCTCCCGGACACACTTCGAGGCGGAGTGTGTGAGCGCGCGCGCTGTAC	780
Db	721	TTCCGCGGCATCTCCCGGACACACTTCGAGGCGGAGTGTGTGAGCGCGCGCGCTGTAC	780
Qy	781	TATTACGAAACGCGCGCCGCTGTACTACCGGCTTTCGTGCGAAGCGGGCGCGGCTG	840
Db	781	TATTACGAAACGCGCGCCGCTGTACTACCGGCTTTCGTGCGAAGCGGGCGCGGCTG	840
Qy	841	GCTACTGTGCGAACAATTTTCCCGCGGATCAGGAAGTACGAGGGGCGCTCGAGCC	900
Db	841	GCTACTGTGCGAACAATTTTCCCGCGGATCAGGAAGTACGAGGGGCGCTCGAGCC	900
Qy	901	ACCACCGGTTTATCTTGACAAACCCCGGGTGTGTACCTTCGGCTGGTACCGCTCAAG	960
Db	901	ACCACCGGTTTATCTTGACAAACCCCGGGTGTGTACCTTCGGCTGGTACCGCTCAAG	960
Qy	961	CCCGCGCGGGAAACCGCGCGCCCAACCGCGCCCGACCGCGCTTCGGAACCTCGAGC	1020
Db	961	CCCGCGCGGGAAACCGCGCGCCCAACCGCGCCCGACCGCGCTTCGGAACCTCGAGC	1020
Qy	1021	GAGCTCGAGTTTAACTGACGCGGACCACTGGCGTTCGAGGGGGCCATGTGTGACCTG	1080
Db	1021	GAGCTCGAGTTTAACTGACGCGGACCACTGGCGTTCGAGGGGGCCATGTGTGACCTG	1080
Qy	1081	CCGGCTTACAGCTCATGTGCTTCGATATCGAATGCAAGCCCGGGGGAGGACGAGCTG	1140
Db	1081	CCGGCTTACAGCTCATGTGCTTCGATATCGAATGCAAGCCCGGGGGAGGACGAGCTG	1140
Qy	1141	GCCTTTCCGCTCGGAAACCGCGGAGACCTCGTATCCAGATCTCTGCTGTCTTAC	1200
Db	1141	GCCTTTCCGCTCGGAAACCGCGGAGACCTCGTATCCAGATCTCTGCTGTCTTAC	1200
Qy	1201	GACGTGACACCGCGCTTCGAGCATCTCTGTTTCGTCGATTCCTCGGACCTC	1260
Db	1201	GACGTGACACCGCGCTTCGAGCATCTCTGTTTCGTCGATTCCTCGGACCTC	1260
Qy	1261	CCGAGTCCACCTCAGCGATCTCGCTCCAGGGGCTCGCGGCCCGCTCGCTCGGAG	1320
Db	1261	CCGAGTCCACCTCAGCGATCTCGCTCCAGGGGCTCGCGGCCCGCTCGCTCGGAG	1320
Qy	1321	TTTGACAGGAAATTCGAGATGCTGCTGCGCTTCATGACCTTCGTTCAGGAGTACGGCCC	1380
Db	1321	TTTGACAGGAAATTCGAGATGCTGCTGCGCTTCATGACCTTCGTTCAGGAGTACGGCCC	1380
Qy	1381	GAGTTCGTGACGGGTACACATCATCTCGACTGCGCTTCGTCCTGACCAAGCTG	1440
Db	1381	GAGTTCGTGACGGGTACACATCATCTCGACTGCGCTTCGTCCTGACCAAGCTG	1440
Qy	1441	ACGAGATCTACAAAGTCCCGCTCGACGGGTACGGGCGCATGAACCGCGCGGGTGTTC	1500
Db	1441	ACGAGATCTACAAAGTCCCGCTCGACGGGTACGGGCGCATGAACCGCGCGGGTGTTC	1500
Qy	1501	CGCGTGTGGACATCGCGCCAGAGCCATTTTCAGAGCGCAGCAAGATCAAGGTGAACGG	1560
Db	1501	CGCGTGTGGACATCGCGCCAGAGCCATTTTCAGAGCGCAGCAAGATCAAGGTGAACGG	1560
Qy	1561	ATGCTGAAACATGACATGTACGGCATCATCACGCAAGGTCAAACTCTCCAGCTCAAG	1620
Db	1561	ATGCTGAAACATGACATGTACGGCATCATCACGCAAGGTCAAACTCTCCAGCTCAAG	1620
Qy	1621	CTGAAACCGCGCTCGCGGAGCGCTCTTGAAGGACAAAGAAAGGATCTGAGCTACCGGAC	1680
Db	1621	CTGAAACCGCGCTCGCGGAGCGCTCTTGAAGGACAAAGAAAGGATCTGAGCTACCGGAC	1680
Qy	1681	ATCCCCCGCTTACAGCTTCGGCGCGCGAGCGGGGTGATCGCGGAGTATTGTGTG	1740
Db	1681	ATCCCCCGCTTACAGCTTCGGCGCGCGAGCGGGGTGATCGCGGAGTATTGTGTG	1740
Qy	1741	CAGGACTCGCTGCTGGTGGGAGCTTCTTCAAGTTTCTGCGCGACCTTGGAGCTTTC	1800
Db	1741	CAGGACTCGCTGCTGGTGGGAGCTTCTTCAAGTTTCTGCGCGACCTTGGAGCTTTC	1800

Qy	1801	GCCGTCGGCGCGCTTGGCGGGGATCAACATCAACCCGCGACCATCTATAGACGGCGACGACATC	1861
Db	1801	GCCGTCGGCGCGCTTGGCGGGGATCAACATCAACCCGCGACCATCTATAGACGGCGACGACATC	1860
Qy	1861	CGCGCTTTCAGCTGCTCTCGCGCTTGGCGGGCCAGAAAGGCTTCATCTCTGCCGGACACC	1920
Db	1861	CGCGCTTTCAGCTGCTCTCGCGCTTGGCGGGCCAGAAAGGCTTCATCTCTGCCGGACACC	1920
Qy	1921	CAGGGGCGGTTTTCGGGCGCTTCGAACAAGAGGCGCCCAAGCGCCCGCGCTTGGTACCG	1980
Db	1921	CAGGGGCGGTTTTCGGGCGCTTCGAACAAGAGGCGCCCAAGCGCCCGCGCTTGGTACCG	1980
Qy	1981	GAAGGGGAGCGCGCGGGGACGGGAAACGGGGACGAGGTAAGNACGACGACGAGGACGAG	2040
Db	1981	GAAGGGGAGCGCGCGGGGACGGGAAACGGGGACGAGGTAAGNACGACGACGAGGACGAG	2040
Qy	2041	GACGGGACGAGACCGCAGGAGGTCCGCGCGAGACCGGGGCGCGGACGCTTGGGTACCG	2100
Db	2041	GACGGGACGAGACCGCAGGAGGTCCGCGCGAGACCGGGGCGCGGACGCTTGGGTACCG	2100
Qy	2101	GGGGCCCGGGTCTCGACCCCACTCCGGGTTCACGTGCAACCCGCTGGTGGTTCAGTACGCTCTCC	2160
Db	2101	GGGGCCCGGGTCTCGACCCCACTCCGGGTTCACGTGCAACCCGCTGGTGGTTCAGTACGCTCTCC	2160
Qy	2161	TTTTGCCAGCTGTACCCCGACCATCATCGAGGCCCAAACTGTGCTTCAGTACGCTCTCC	2220
Db	2161	TTTTGCCAGCTGTACCCCGACCATCATCGAGGCCCAAACTGTGCTTCAGTACGCTCTCC	2220
Qy	2221	CTGGGGCCCGAGGCGCTCGGCGACCTCGAGGCGGACCGGGACCTACCTGGAGATCGAGGTG	2280
Db	2221	CTGGGGCCCGAGGCGCTCGGCGACCTCGAGGCGGACCGGGACCTACCTGGAGATCGAGGTG	2280
Qy	2281	GGGGGCCGACGGCTGTTCTTCGTGAAGGCCCAACGTACGCGAGAGCCCTGCTGAGCATCCTG	2340
Db	2281	GGGGGCCGACGGCTGTTCTTCGTGAAGGCCCAACGTACGCGAGAGCCCTGCTGAGCATCCTG	2340
Qy	2341	CTGGCGCATGCTGGCGCATCGGAAAGCAGATCCGCTCGCGGATCCCCACAGACGCCCC	2400
Db	2341	CTGGCGCATGCTGGCGCATCGGAAAGCAGATCCGCTCGCGGATCCCCACAGACGCCCC	2400
Qy	2401	GAGGAGGCGCTCTCTCGACAGACACAGGCGCCCATCAAGGTGGTGTGCAACTCGGTG	2460
Db	2401	GAGGAGGCGCTCTCTCGACAGACACAGGCGCCCATCAAGGTGGTGTGCAACTCGGTG	2460
Qy	2461	TACGGGTTCACCGGGCGCAGCAGGTCTTCTGCGCTCCCTGCACTGGCGCGCCACCGCTG	2520
Db	2461	TACGGGTTCACCGGGCGCAGCAGGTCTTCTGCGCTCCCTGCACTGGCGCGCCACCGCTG	2520
Qy	2521	ACGACATACGGCGCGCAGATGCTCTTCGCGACGCGCGCGTACGTGACGCGCTGGGGG	2580
Db	2521	ACGACATACGGCGCGCAGATGCTCTTCGCGACGCGCGCGTACGTGACGCGCTGGGGG	2580
Qy	2581	GAGTTGCATCAGCTGTGGCGCATTTTCGGAGGCGCGCGGCATGCGCGCCCCCGGTCCG	2640
Db	2581	GAGTTGCATCAGCTGTGGCGCATTTTCGGAGGCGCGCGGCATGCGCGCCCCCGGTCCG	2640
Qy	2641	TACTCCATCGGCATCATCTACGGGGACACGCACTTCATTTTGTGTCGCCCGGCGCTC	2700
Db	2641	TACTCCATCGGCATCATCTACGGGGACACGCACTTCATTTTGTGTCGCCCGGCGCTC	2700
Qy	2701	ACGGCCCGGGCCTGTGGCCATCTGGGCGACAAGATGGCGAGCCACATCTCGCGCGCGCTG	2760
Db	2701	ACGGCCCGGGCCTGTGGCCATCTGGGCGACAAGATGGCGAGCCACATCTCGCGCGCGCTG	2760
Qy	2761	TTCTCTCCCCCGCATCAAGCTCGAGTGGGAAAAAAGCTTACCAAGCTGTGCTCATCGCC	2820
Db	2761	TTCTCTCCCCCGCATCAAGCTCGAGTGGGAAAAAAGCTTACCAAGCTGTGCTCATCGCC	2820
Qy	2821	AAGAAAAAGTACATCGCGCTCATCTCGGGGGCAAGATGCTCATCAAGGGCGGTGATCTG	2880
Db	2821	AAGAAAAAGTACATCGCGCGTTCATCTCGGGGGCAAGATGCTCATCAAGGGCGGTGATCTG	2880
Qy	2881	GTGCGCAAAACAACTCGCGCGTTTATCAACCGCACCTTCAGAGGCGCCCTGGTTCGACCTGCTG	2940

[illegible]

## RESULT 2

AAD30078  
ID AAD30078 standard; DNA; 3723 BP.

AC AAD30078;

DT 17-MAY-2002 (first entry)

DE Herpes simplex virus (HSV2-186-M1) mutant DNA polymerase gene.

XX Herpes virus; medicinal; therapy; binding domain; DNA polymerase gene;  
KW

XX  
antiviral; enzyme; mutant; ds.

OS Herpes simplex virus.

XX	Key	Location/Qualifiers
FH		

FT	key	location
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/*tag= a
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WO200206513-A2.

24-JAN-2002.

13-JUL-2001; 2001WO-US016525.

13-JUL-2000; 2000US-0218118P.

13-APR-2001; 2001US-0283880P.

( PHAA ) PHARMACIA & UPJOHN CO.

Homa FL, Wathen MW, Hopkins TA, Thomsen DR;

WPI; 2002-179800/23.

P-PSDB; AAE18854.

Selecting compounds that inhibit herpes viruses by comparing inhibitory concentration of a compound of interest that inhibits wild-type herpes virus and domain mutant herpes virus, and selecting compound of interest.

Claim 25; Fig 5; 126pp; English.

The present invention relates to a method for selecting compounds that inhibit herpes viruses. The method involves measuring IC<sub>50</sub> of compound of interest that inhibits wild-type herpes virus and domain mutant herpes virus mutant herpes virus which is the same strain as wild-type herpes virus, comparing IC<sub>50</sub> of the compound inhibiting wild-type herpes virus with IC<sub>50</sub> of the compound inhibiting mutant herpes virus and selecting the compound, where IC<sub>50</sub> of the compound of interest that inhibits mutant herpes virus is at least 3 times greater than IC<sub>50</sub> of the compound that inhibits wild-type herpes virus. The method is useful for selecting compounds that inhibit herpes viruses. The compound is useful for manufacture of medicinals for selectively treating diseases caused by herpes viruses such as herpes viral infection, or for selectively inhibiting herpes viruses, in a human host by administering a compound to human in need of such treatment, where the compound inhibits herpes viruses by interaction with the binding domain in the viral DNA polymerase, and IC<sub>50</sub> of the compound that inhibits a binding domain mutant herpes virus is at least 3 times, preferably 5 times greater than IC<sub>50</sub> of the compound that inhibits the wild-type herpes virus which is the same strain as the mutant herpes virus. The present sequence is Herpes simplex virus (HSV2-186-M1) mutant DNA polymerase gene

Sequence 3723 BP; 625 A; 1295 C; 1206 G; 597 T; 0 U; 0 Other;

Query Match 99.4%; Score 3696.2; DB 6; Length 3723;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 3714; Conservative 0; Mismatches 3; Indels 6; Gaps 1;

Qy 1 ATGTTTGTGCGCGGCGGCCGACTTCCCCGGGGGAAGTCGGCGGCTCGGGCGCG 60

Db  
1 ATGTTTGTCCGCGGCGGCCGGCTTCCCCGGGGGAAGTCGGCGGCTCGGGCGCG 60

61 TCTGGGTTTTTGTGCCCCCCCACAACCCCCGGGGAGCCACCCAGACGGCACCGCCGCTTGC 120

db 61 TCTGGGTTTTTGTGCCCCCAACCCCGGGGAGCCACCCAGACGGCACCGCCGCCTTGC 120

121 CGCCGGCAGAACTTCTACAACCCCCACCTCGCTCAGACCGGAACGCAGCCAAAGGCCCCC 180

121 CGCCGGCAGAACTTCTTCAACCCCA CCTCGCTCAGACCGGAACGCA GCCAAGGCCCCC 180

181 GGGCCGECTCAGCGCCATACGTACTACAGCGAGTGCAGCGAATTTTCGATTTATCGCCCCCG 240

db 181 GGGCCGGCTCAGCGCCATA CGTACTACAGCGAGTGGCAGCGAA TTTTCGATTATCGCCCCG 240

OV 241 CGTTCGCTGGACGAGGACGCCCGCGGAGCAGCGCACCGGGGTCCACGACGGCGCGCTC 300

Db 241 CGTTGGTGGACGAGGACGCCCCCGCGGAGCAGCGCACCGGGTCCACGACGGCCGGCTC 300

301 CGGCGCGCCCCCTAAGGTGTA CTGCGGGGGGA CGAGCGGACGTCTCCGCGTGGGCCCG 360



Db 1381 GAGTTCTGACCGGGTACAACATCATCACTTCGACTGSCCTTCTGCTCTGACCAAGCTG 1440  
Qy 1441 ACGGAGATTCTAAGTCCCGCTCGACGGGTACGGGCGCATGAACGGCGGGGGTGTTC 1500  
Db 1441 ACGGAGATTCTAAGTCCCGCTCGACGGGTACGGGCGCATGAACGGCGGGGGTGTTC 1500  
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Db 1621 CTGAACGCGCTCGCCGAGCGCTCTTGAAGGACAAAGAAAGGATCTGAGCTACCGGAC 1680  
Qy 1681 ATCCCGCCTACTACGCTCTCGGCGCCGCGCAGCGCGGGGTGATCGGCGAGTATTGTGTG 1740  
Db 1681 ATCCCGCCTACTACGCTCTCGGCGCCGCGCAGCGCGGGGTGATCGGCGAGTATTGTGTG 1740  
Qy 1741 CAGGACTCGCTGCTGCTCGGCGAGCTGTTCTTCAAGTTTCTGCGGACCTTCC 1800  
Db 1741 CAGGACTCGCTGCTGCTCGGCGAGCTGTTCTTCAAGTTTCTGCGGACCTTCC 1800  
Qy 1801 GCCGTGCGCGCTCGGCGGCGCATCAACATCAACCGCACCATCTACGACGGCCACGATC 1860  
Db 1801 GCCGTGCGCGCTCGGCGGCGCATCAACATCAACCGCACCATCTACGACGGCCACGATC 1860  
Qy 1861 CGCGTCTTCACTGCTCTCGGCTTTCGGGCGCAGAAAGGCTTCACTCTCGCGGACAC 1920  
Db 1861 CGCGTCTTCACTGCTCTCGGCTTTCGGGCGCAGAAAGGCTTCACTCTCGCGGACAC 1920  
Qy 1921 CAGGGCGGTTTCGGGCGCTCGACAAAGAGCGCCCAAGCGCCCGGCTGCTCGGGG 1980  
Db 1921 CAGGGCGGTTTCGGGCGCTCGACAAAGAGCGCCCAAGCGCCCGGCTGCTCGGGG 1980  
Qy 1981 GAAGGGAGCGCGCGGGGCGGGAACGGGGACGAGATAGGACGACGACGA-----G 2034  
Db 1981 GAAGGGAGCGCGCGGGGCGGGAACGGGGACGAGATAGGACGAGGACGGG 2040  
Qy 2035 GACGAGGACGGGGACGAGCGCGAGGAGTTCGCGCGAGACCGGGGGCGGACGTTGGG 2094  
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Qy 2095 TACAGGGGGCGCGGCTCTCGACCCACCTTCGGGTTTCACTGCGACCCCGTGGTGGT 2154  
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Qy 2155 TTTGACTTTGCGACGCTGTACCCAGCATCATCCAGGCGCCACCACTGTGCTTCAGTACG 2214  
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Db 2221 CTCTCCCTGCGGCGCGGCGCTCGCGCCTCTGAGGCGGACCGGGACTACTCTGAGATC 2280  
Qy 2275 GAGTGGGGGCGCAGCGCTGTTCTTGTGAAGGCCCACTGACGCGAGAGCTGCTGAGC 2334  
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Qy 2395 ACCCCCGAGGAGCGGCTCTCTCGACAAAGCAACAGCGCGCCATCAAGGTGGTGTCAAC 2454  
Db 2401 CCCCCCGAGGAGCGGCTCTCTCGACAAAGCAACAGCGCGCCATCAAGGTGGTGTCAAC 2460  
Qy 2455 TCGGTGTACGGGTTTCAACGGGGCGCAGCAGGTTCTTGTGCTTCTGCTGCTGCTGCGGCGCC 2514  
Db 2461 TCGGTGTACGGGTTTCAACGGGGCGCAGCAGGTTCTTGTGCTTCTGCTGCTGCTGCGGCGCC 2520

Qy 2515 ACCGTGACGACCATCGGCCGCGAGATGCTCTCTCGCAGCGCGCGTACGTGACGCGCGC 2574  
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Qy 2695 GGCCTCACGCGCGCGGCGCTGCTGGCCATGCGGCGCAAGATGCGGAGCCACATCTCGGCG 2754  
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Qy 2755 GCGCTGTTCTCTCCCGCATCAAGCTCGAGTTCGAAAGAAAGTTCACCAAGCTCTGCTC 2814  
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Db 3001 GAGGAGTGGCTGCGGCGACCCCTGCGCGAGGAGTTCGAGGGTTCGCGGGCGCTCTCGTA 3060  
Qy 3055 GAGCCCATCGCGCATCACGACCGCGAGGAGGATCCAGGACTTTGCTTCAACGCGC 3114  
Db 3061 GAGCCCATCGCGCATCACGACCGCGAGGAGGATCCAGGACTTTGCTTCAACGCGC 3120  
Qy 3115 GAACTGAGCAGACACCGCGCGGTACACAAAGCGCTTCGCCCACTGACGGTGTAT 3174  
Db 3121 GAACTGAGCAGACACCGCGCGGTACACAAAGCGCTTCGCCCACTGACGGTGTAT 3180  
Qy 3175 TACAGCTATGCGCGCGCGAGTCCCGTCCATCAAGNACCGGATCCGTAAGTCCGTAAGT 3234  
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Db 3301 CTAGAGCGCGCGCGCGGAGCGAGCCCGCGCGCGCGCGCGCTTCCGCTCCCGCGCC 3360  
Qy 3355 AAGGGCCCCCGGAGAGCGCTGCGATGCGACCCCGCGGAGGCGGCTCCAGCGCGCC 3414  
Db 3361 AAGGGCCCCCGGAGAGCGCTGCGATGCGACCCCGCGGAGGCGGCTCCAGCGCGCC 3420  
Qy 3415 AAGCTGCTGTGTTCCGAGTTCGCGGAGTCCCGGGTACCGCATTCGCGCGGGGGTTCG 3474  
Db 3421 AAGCTGCTGTGTTCCGAGTTCGCGGAGTTCGCGGAGTTCGCGCATTCGCGCGGGGGTTCG 3480  
Qy 3475 CTCAACGCGACTATTACTTCTCGCACCTGCTGGGGCGGCTGCTGCTGAGCTTCAAGGCC 3534  
Db 3481 CTCAACGCGACTATTACTTCTCGCACCTGCTGGGGCGGCTGCTGCTGAGCTTCAAGGCC 3540  
Qy 3535 CTGTTTGGAAATAACCGCAAGATCACCGAGTCTGTTTAAAGAGGTTTATTTCCGAGAGC 3594  
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QY 601 GGCACGGCGAGTACTTTTACATGAACAAGCGGAGGTGGATCGGCACCTCGAGTGCCT 660  
DB 6870 GGCACGGCGAGTACTTTTACATGAACAAGCGGAGGTGGATCGGCACCTCGAGTGCCT 6929  
QY 661 GCGCCGCGCGATCTCTGCGAGCGCTGCGGGCGCCCTGCGGAGTGCCTCGGGGCGCTG 720  
DB 6930 GCGCCGCGCGATCTCTGCGAGCGCTGCGGGCGCCCTGCGGAGTGCCTCGGGGCGCTG 6989  
QY 721 TTCGCGCGATCTCTCGCGGACCACTTCGAGCGGAGGTGGTGGAGCGCGCGACGTGTAC 780  
DB 6990 TTCGCGCGATCTCTCGCGGACCACTTCGAGCGGAGGTGGTGGAGCGCGCGACGTGTAC 7049  
QY 781 TATTACGAAACCGCGCCGACCTGTATCTACCGCTCTTCGTGCGAAGCGGCGCGCGCTG 840  
DB 7050 TATTACGAAACCGCGCCGACCTGTATCTACCGCGCTCTTCGTGCGAAGCGGCGCGCGCTG 7109  
QY 841 GCCTACCTGTGCGACAACTTTTCCCGCGGATCAGGAGTACGAGGGGGGCGTGCAGCC 900  
DB 7110 GCCTACCTGTGCGACAACTTTTCCCGCGGATCAGGAGTACGAGGGGGGCGTGCAGCC 7169  
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DB 7230 CCGGCGCGGGAAACGCGCGCGCCCAACCGCGCCCGCGACGCGGTTTCGGAACCTCGAGC 7289  
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DB 7290 GACGTGCGAGTTTAACTGCACGCGCGACAACTTGGCGCTGAGGGGGCCATGTGTGACCTG 7349  
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DB 7710 ACGGAGATCTAAAGTCTCCGCTCGACGGGTACCGGCGCATGAACCGCGGGTGTCTTC 7769  
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QY 1681 ATCCCCGCTACTACGCTCTCGGGCCCGCGAGCGCGGGGTGATCGCGGAGTATTGTGTG 1740

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DB 8670 ACCCCGAGGAGGCGGCTCTCTCGAACAAAGGCCGCCATCAAGGTGGTGTGCAAC 8729  
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Qy 3655 GCCGGCGCTACGGCGGAGGAACTCGTTCGAATGTTGATAGAGCTTTGATCTCTAGCA 3714

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Qy 3715 TGA 3717

Db 9990 TGA 9992

RESULT 4  
AAV62176  
ID AAV62176 standard; DNA; 117213 BP.  
XX AC AAV62176;  
XX

DT 13-JAN-1999 (first entry)

XX HSV-2 strain SB5 Contig ID 15 DNA sequence.

DE HSV-2 strain SB5; immunological response induction; therapy;

XX antiviral identification; viral protein inhibitor; ss.

KW Herpes simplex virus 2.

OS

XX

PH Location/Qualifiers

CDS 755..1297

FT /\*tag= a

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FT /note= "encoded protein shown in AAW72170"

FT 1170..2174

FT /\*tag= b

FT /product= "ORF#2 protein"

FT /note= "encoded protein shown in AAW72171"

FT 2229..2930

FT /\*tag= c

FT /product= "ORF#3 protein"

FT /note= "encoded protein shown in AAW72172"

FT complement(3130..3735)

FT /\*tag= d

FT /product= "ORF#4 protein"

FT /note= "encoded protein shown in AAW72173"

FT complement(3802..6447)

FT /\*tag= e

FT /product= "ORF#5 protein"

FT /note= "encoded protein shown in AAW72174"

FT 6017..8482

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FT /product= "ORF#6 protein"

FT /note= "encoded protein shown in AAW72250"

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FT /\*tag= j

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FT /product= "ORF#6b protein"

FT /note= "encoded protein shown in AAW72245"

FT 6446..8482

FT /\*tag= l

FT /product= "ORF#6a protein"

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FT /transl\_except= (pos: 7481..7486, aa: Ile)

FT /note= "encoded protein shown in AAW72244"

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FT /\*tag= m

FT /product= "ORF#7 protein"

FT /note= "encoded protein shown in AAW72175"

FT complement(9604..11855)

FT /\*tag= n

FT /transl\_except= (pos: 11635..11636, aa: Ala)

FT /product= "ORF#8 protein"

FT /note= "encoded protein shown in AAW72176"

FT complement(11905..14520)

FT /\*tag= p

FT /product= "ORF#9a protein"

FT /note= "encoded protein shown in AAW72223"

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Qy	301	CGCGCGCCCTTAAGGTGTAAGTCTCGGGGGGAGCGAGCGACGCTCTCTCGCGTGGCCCG	360	Db	55773	GAGTTGCTGACCGGGTACAACATCATCACTTTCGACTGGCCCTTCGCTCTGACCAAGCTG	55832
Db	54693	CGCGCGCCCTTAAGGTGTAAGTCTCGGGGGGAGCGAGCGACGCTCTCTCGCGTGGCCCG	54752	Qy	1441	ACGAGAGATCTACAAGGTCCCGCTCGACGGGTACGGGCGCATGAACCGCGGGGTGTTC	1500
Qy	361	GAGGGCTTCTGGCGCGCTCGCTTGGGGCGGTGCGAACCATGCCCCCAAGGGG	420	Db	55833	ACGAGAGATCTACAAGGTCCCGCTCGACGGGTACGGGCGCATGAACCGCGGGGTGTTC	55892
Db	54753	GAGGGCTTCTGGCGCGCTCGCTTGGGGCGGTGCGAACCATGCCCCCGAGGGG	54812	Qy	1501	CGGCTGGGAGCATCGGCGAGAGCACTTTTCAGAACGCGAGCAAGATCAAGTGAACGG	1560
Qy	421	TTGACCCCAACGCTACCGTCTTCCAGTGTACGACATCTTGAGCACTGGAACACGCG	480	Db	55893	CGGCTGGGAGCATCGGCGAGAGCACTTTTCAGAACGCGAGCAAGATCAAGTGAACGG	55952
Db	54813	TTGACCCCAACGCTACCGTCTTCCAGTGTACGACATCTTGAGCACTGGAACACGCG	54872	Qy	1561	ATGCTCAACATCGACATGTACGCGCATCATCACGACAAAGTCAAACTCTCCAGCTACAAG	1620
Qy	481	TACAGCATGCGCGCGCCAGCTCCAGAGGATTTATGACGCCATCAAGCCCGCGGG	540	Db	55953	ATGCTCAACATCGACATGTACGCGCATCATCACGACAAAGTCAAACTCTCCAGCTACAAG	56012
Db	54873	TACAGCATGCGCGCGCCAGCTCCAGAGGATTTATGACGCCATCAAGCCCGCGGG	54932	Qy	1621	CTGAACCGCGCTCGCGAGGCGGTCTTTGAAGGCAAGAAAGGATCTGAGCTACCGGAC	1680
Qy	541	ACGCTCATACGCTTCTGGGTCTGACCCCGAAGGCCATCGCGTCCGCGTTACAGCTAC	600	Db	56013	CTGAACCGCGCTCGCGAGGCGGTCTTTGAAGGCAAGAAAGGATCTGAGCTACCGGAC	56072
Db	54933	ACGCTCATACGCTTCTGGGTCTGACCCCGAAGGCCATCGCGTCCGCGTTACAGCTAC	54992	Qy	1681	ATCCCCCGCTACTACGCGCTCGGGCCCGCGAGCGGGGTGATCGGCGAGTATTGTG	1740
Qy	601	GGCACGCGGAGTACTTTTATGAAACAAAGCGGAGGTGATCGGCACTTGCAGTGCCT	660	Db	56073	ATCCCCCGCTACTACGCGCTCGGGCCCGCGAGCGGGGTGATCGGCGAGTATTGTG	56132
Db	54993	GGCACGCGGAGTACTTTTATGAAACAAAGCGGAGGTGATCGGCACTTGCAGTGCCT	55052	Qy	1741	CAGGACTCGCTGCTGCTCGGGCAGCTGTTCTTCAAGTCTTTCGCGCACCTTGGAGCTTTC	1800
Qy	661	GCCCCGCGCATCTCTCGAGCGCTTGGCGCGCCCTGCGAGTCCGCGGGGGGTG	720	Db	56133	CAGGACTCGCTGCTGCTCGGGCAGCTGTTCTTCAAGTCTTTCGCGCACCTTGGAGCTTTC	56192
Db	55053	GCCCCGCGCATCTCTCGAGCGCTTGGCGCGCCCTGCGAGTCCGCGGGGGGTG	55112	Qy	1801	GCGCTCGCGCTCGCGGCGCATCAACATCACCGCACCATCTA	1860
Qy	721	TTCCGCGGCATCTCCGCGACCACTTCGAGCGAGGTGATGAGCGCGCGACGCTGAC	780	Db	56193	GCGCTCGCGCTCGCGGCGCATCAACATCACCGCACCATCTA	56252
Db	55113	TTCCGCGGCATCTCCGCGACCACTTCGAGCGAGGTGATGAGCGCGCGACGCTGAC	55172	Qy	1861	CGGCTCTTCACTGCTCTCTGCGCTTGGGGCAGAAAGGCTTCTATCTCCGCGACACC	1920
Qy	781	TATTAAGAAACGCGCCCGAACCTGTACTACCGGTCTTCTGTGGAAGCGGCGCGCTG	840	Db	56253	CGGCTCTTCACTGCTCTCTGCGCTTGGGGCAGAAAGGCTTCTATCTCCGCGACACC	56312
Db	55173	TATTAAGAAACGCGCCCGAACCTGTACTACCGGTCTTCTGTGGAAGCGGCGCGCTG	55232	Qy	1921	CAGGGCGGTTTTCGCGGCTCTCGAACAGGAGGCGCCCAAGCGCGCGCGCTCTCGGGG	1980
Qy	841	GCTTACTGTGCGACAACTTTTCCCGCGCATCAGGAAGTACGAGGGGGCGTCCAGCC	900	Db	56313	CAGGGCGGTTTTCGCGGCTCTCGAACAGGAGGCGCCCAAGCGCGCGCTCTCGGGG	56372
Db	55233	GCTTACTGTGCGACAACTTTTCCCGCGCATCAGGAAGTACGAGGGGGCGTCCAGCC	55292	Qy	1981	GAAGGGAGCGGCGCGGGGAGCGGGAACGGGGAACGAGGATTAAGAACGACGACGA	2034
Qy	901	ACCACCGGTTTATCTTGGAACAACCGGGGTGTTGACCTTTCGGCTGCTGACCGCTCAAG	960	Db	56373	GAAGGGAGCGGCGCGGGGAGCGGGAACGGGGAACGAGGATTAAGAACGACGACGACGA	56432
Db	55293	ACCACCGGTTTATCTTGGAACAACCGGGGTGTTGACCTTTCGGCTGCTGACCGCTCAAG	55352	Qy	2035	GACGAGACGGGGAACGAGCGCGAGGAGGTGCGCGGAGACCGGGGCGCGGACGTTGGG	2094
Qy	961	CCGCGCGCGGGAACGCGCGCGGCGCAACCGCGCCCGCGCGGCTTCGGAACCTCGAGC	1020	Db	56433	GACGAGACGGGGAACGAGCGCGAGGAGGTGCGCGGAGACCGGGGCGCGGACGTTGGG	56492
Db	55353	CCGCGCGCGGGAACGCGCGCGGCGCAACCGCGCCCGCGCGGCTTCGGAACCTCGAGC	55412	Qy	2095	TACGAGGGGCGCGCGGCTCTCGACCCCACTCCTCGGGTTCACGTCGACCCCGTGGTGGT	2154
Qy	1021	GAGTCTGAGTTTAAGTCAAGCGGGAACAACCTGCGCTCGAGGGGGCATGTGTACCTG	1080	Db	56493	TACGAGGGGCGCGCGGCTCTCGACCCCACTCCTCGGGTTCACGTCGACCCCGTGGTGGT	56552
Db	55413	GAGTCTGAGTTTAAGTCAAGCGGGAACAACCTGCGCTCGAGGGGGCATGTGTACCTG	55472	Qy	2155	TTTGAATTTGCCAGCTGCTGACCCAGGATCATCCAGGCGCAACACCTGTGCTTCAGTACG	2214
Qy	1081	CCGCGCTTCAAGCTCATGTGCTTCGATATCGAATGCAAGCCCGGGGGAGGACGAGCTG	1140	Db	56553	TTTGAATTTGCCAGCTGCTGACCCAGGATCATCCAGGCGCAACACCTGTGCTTCAGTACG	56612
Db	55473	CCGCGCTTCAAGCTCATGTGCTTCGATATCGAATGCAAGCCCGGGGGAGGACGAGCTG	55532	Qy	2215	CTCTCCTCGGGCCGAGCGGCTCGGCACTTGGAGGCGGACCGGGACTACCTTGGAGATC	2274
Qy	1141	GCCTTTCGGTGGGGAACGCGCGGGAAGACCTGCTCATTCAGATCTCTGCTGCTCTAC	1200	Db	56613	CTCTCCTCGGGCCGAGCGGCTCGGCACTTGGAGGCGGACCGGGACTACCTTGGAGATC	56672
Db	55533	GCCTTTCGGTGGGGAACGCGCGGGAAGACCTGCTCATTCAGATCTCTGCTGCTCTAC	55592	Qy	2275	GAGTGGGGGGCGAGCGGCTGTTCTTCTGTAAGGGCCACGTCAGCGAGAGCTCTGCTGAGC	2334
Qy	1201	GACTGTCCACACCGCCCTCGAGCACAACCTCTGTTTTCGCTCGGATCTCTCGACCTC	1260	Db	56673	GAGTGGGGGGCGAGCGGCTGTTCTTCTGTAAGGGCCACGTCAGCGAGAGCTCTGCTGAGC	56732
Db	55593	GACTGTCCACACCGCCCTCGAGCACAACCTCTGTTTTCGCTCGGATCTCTCGACCTC	55652	Qy	2335	ATCCTGCTGCGAGCTGCGCATCGGCAAGAGAGATCGGCTCGCGGATCCCGCAGAGC	2394
Qy	1261	CCGAGTCCCACTCAGCGATCTCGCTCCAGGGGCTGCGCGCCCGCTGCTCTGAGAG	1320	Db	56733	ATCCTGCTGCGAGCTGCGCATCGGCAAGAGAGATCGGCTCGCGGATCCCGCAGAGC	56792
Db	55653	CCGAGTCCCACTCAGCGATCTCGCTCCAGGGGCTGCGCGCCCGCTGCTCTGAGAG	55712	Qy	2395	ACCCCGAGGAGCGCTCTCTCTCGAAGAGCAACAGCGCGCCCATCAAGGTGGTGTCAAC	2454
Qy	1321	TTTGAAGCGAATTCGAGATCTGCTGCTTCAATGACCTTCTCAAGGAGTACGGCCCC	1380	Db	56793	ACCCCGAGGAGCGCTCTCTCTCGAAGAGCAACAGCGCGCCCATCAAGGTGGTGTCAAC	56852
Db	55713	TTTGAAGCGAATTCGAGATCTGCTGCTTCAATGACCTTCTCAAGGAGTACGGCCCC	55772				



Qy 2455 TCGGTGTAACGGTTTACCGGGCGCAGCAAGGTCTTCTGCGCTGCTGCAAGTGGCGGCC 2514  
Db 56953 TCGGTGTACGGTTTACCGGGTGCAGACAGGTCTTCTGCGCTGCTGCAAGTGGCGGCC 56912  
Qy 2515 ACCGTGACGACATCGCGCGGAGATGCTCTCGCGACGCGCGGTGAGTGCACGCGGC 2574  
Db 56913 ACCGTGACGACATCGCGCGGAGATGCTCTCGCGACGCGCGGTGAGTGCACGCGGC 56972  
Qy 2575 TGGCGGAGTTTCGATCAGCTGCTGCGCGACTTTCCGAGGGCGCGCGCATGCGCGCCCC 2634  
Db 56973 TGGCGGAGTTTCGATCAGCTGCTGCGCGACTTTCCGAGGGCGCGCGCATGCGCGCCCC 57032  
Qy 2635 GGTCCGTAATCCATCGCGCATCATCTACGGGACACGCACTCCATTTTGTGTCGCG 2694  
Db 57033 GGTCCGTAATCCATCGCGCATCATCTACGGGACACGCACTCCATTTTGTGTCGCG 57092  
Qy 2695 GGCCTACGGCGCGCGCTGCTGGCCATGCGGCGCAAGATGGCGAGCCACATCTCGCGC 2754  
Db 57093 GGCCTACGGCGCGCGCTGCTGGCCATGCGGCGCAAGATGGCGAGCCACATCTCGCGC 57152  
Qy 2755 GCGCTGTTCTCCCGCGATCAAGCTCGAGTGCAGAAAGGTTTCAACAGCTGCTGCTC 2814  
Db 57153 GCGCTGTTCTCCCGCGATCAAGCTCGAGTGCAGAAAGGTTTCAACAGCTGCTGCTC 57212  
Qy 2815 ATGCCAAGAAAGTATCATCGCGTTCATCTCGCGGGCAAGATGCTCATCAAGGGCGTG 2874  
Db 57213 ATGCCAAGAAAGTATCATCGCGTTCATCTCGCGGGCAAGATGCTCATCAAGGGCGTG 57272  
Qy 2875 GATCTGTGCGCAAAACAACTGCGGTTTATCAACCGCACTCCAGGGCGCTGCTGCAC 2934  
Db 57273 GATCTGTGCGCAAAACAACTGCGGTTTATCAACCGCACTCCAGGGCGCTGCTGCAC 57332  
Qy 2935 CTGCTGTTTACGACGATACCGTATCCGAGCGCGCGCGGTTAGCGAGCGCGCCGCA 2994  
Db 57333 CTGCTGTTTACGACGATACCGTATCCGAGCGCGCGCGGTTAGCGAGCGCGCCGCA 57392  
Qy 2995 GAGGAGTGGCTGGCGCAACCTCTCCCGAGGACTGCAAGGCGTTTCGGGGCGCTCCTGTA 3054  
Db 57393 GAGGAGTGGCTGGCGCAACCTCTCCCGAGGACTGCAAGGCGTTTCGGGGCGCTCCTGTA 57452  
Qy 3055 GAGCCCATCGCGCATCAACGACCCGAGAGGACATCCAGGACTTTGCTCCTCACCGCC 3114  
Db 57453 GAGCCCATCGCGCATCAACGACCCGAGAGGACATCCAGGACTTTGCTCCTCACCGCC 57512  
Qy 3115 GAACTGAGCAGACACCGCGCGTACCAACAGCGCTGCGCCACCTGACGGTGTAT 3174  
Db 57513 GAACTGAGCAGACACCGCGCGTACCAACAGCGCTGCGCCACCTGACGGTGTAT 57572  
Qy 3175 TACAAGTCTATGGCCCGCGCGCAGGTCCCGTCCATCAAGGACCGGATCCCGTACGTG 3234  
Db 57573 TACAAGTCTATGGCCCGCGCGCAGGTCCCGTCCATCAAGGACCGGATCCCGTACGTG 57632  
Qy 3235 ATCTGTGCGCAGACCCCGGAGGTAGAGAGACGCTGCGCGGTGCGCGCTCCCGCGAG 3294  
Db 57633 ATCTGTGCGCAGACCCCGGAGGTAGAGAGACGCTGCGCGGTGCGCGCTCCCGCGAG 57692  
Qy 3295 CTAGACCGCGCGCCAGGGAGCGCGCGCCCCCGCGCGCGCTCCCGCGGCC 3354  
Db 57693 CTAGACCGCGCGCCAGGGAGCGCGCGCCCCCGCGCGCGCTCCCGCGGCC 57752  
Qy 3355 AAGCGCCCCGGGAGAGCGCGTCCATGCGCAACCCCGGAGCGCGGTCCAGCGCCCGC 3414  
Db 57753 AAGCGCCCCGGGAGAGCGCGTCCATGCGCAACCCCGGAGCGCGGTCCAGCGCCCGC 57812  
Qy 3415 AAGCTGTGTTCCGAGTGGCGAGATCCCGGGTACGCAATCGCCCCGGGGCGTTCCG 3474  
Db 57813 AAGCTGTGTTCCGAGTGGCGAGATCCCGGGTACGCAATCGCCCCGGGGCGTTCCG 57872  
Qy 3475 CTCAACAGGACTTATTCTCCACCTGCTGGGGGGCGCTCGGTGACGTTCAAGGCC 3534  
Db 57873 CTCAACAGGACTTATTCTCCACCTGCTGGGGGGCGCTCGGTGACGTTCAAGGCC 57932  
Qy 3535 CTGTTTGGAAATAACGCCAAGATCACCGAGAGTCTGTTAAAGAGGTTTATTCCCGAGACG 3594

Db 57933 CTGTTTGGAAATAACGCCAAGATCACCGAGAGTCTGTTAAAGAGGTTTATTCCCGAGACG 57992  
Qy 3595 TGGCACCCCGCGACGACGCTGGCGCGCGGCTCAGGCGCGGGTTTCGGGCCCGCGCGG 3654  
Db 57993 TGGCACCCCGCGACGACGCTGGCGCGCGGCTCAGGCGCGGGTTTCGGGCCCGCGG 58052  
Qy 3655 GCGGCGCTACGCGGAGGAACTCGTCAATGTTGCATAGAGCTTTGATCTACTAGCA 3714  
Db 58053 GCGGCGCTACGCGGAGGAACTCGTCAATGTTGCATAGAGCTTTGATCTACTAGCA 58112  
Qy 3715 TGA 3717  
Db 58113 TGA 58115  
RESULT 5  
AAD25519  
ID AAD25519 standard; DNA; 154746 BP.  
XX AAD25519;  
AC AAD25519;  
XX 26-MAR-2002 (first entry)  
DT Human herpesvirus 2 complete DNA genome.  
XX  
DE Human herpesvirus 2; cytostatic; cancer; immunosuppressive; virucide;  
KW antibacterial; fungicide; protozoicide; antirheumatic; antiinflammatory;  
KW antirheumatic; rheumatoid arthritis; neuroprotective; multiple sclerosis;  
KW immune response; vasotropic; vaccine; gene therapy; autoimmune disease;  
KW vasculitis; ds.  
XX  
OS Human herpesvirus 2.  
XX  
PN WO200176643-A1.  
XX 18-OCT-2001.  
XX 06-APR-2001; 2001WO-US011372.  
XX 07-APR-2000; 2000US-0195680P.  
XX (BAYU ) BAYLOR COLLEGE MEDICINE.  
XX Orson FM, Kinsey BM, Bhogal BS;  
XX WPI; 2002-066308/09.  
XX  
XX Composition for oral delivery of vaccines, comprises expression vector  
containing antigenic genomic sequence, bound to aggregated protein-  
polycationic polymer conjugate or suspension.  
XX  
XX Disclosure; Page 90-132; 145pp; English.  
XX  
XX The invention relates to a composition comprising an expression vector  
bound to an aggregated protein-polycationic polymer conjugate or  
suspension. The expression vector contains a promoter polynucleotide  
sequence operatively linked to a polynucleotide sequence encoding an  
antigen which is a fragment of a gene or genome associated with an  
infectious disease, cancer and autoimmune disease such as rheumatoid  
arthritis, vasculitis, and multiple sclerosis, pathogenic genomes  
consisting of bacterium, fungus, protozoa and virus such as human  
immunodeficiency virus (HIV), herpes simplex virus (HSV), hepatitis C  
virus (HCV), influenza and respiratory syncytial virus (RSV), and  
optionally comprising a nucleotide sequence encoding a cytokine (or a  
cytokine expression vector), is useful for inducing an immune response  
(systemic and/or mucosal) in an organism. The cytokine expression vector  
contains a sequence for granulocyte macrophage-colony stimulating factor  
(GM-CSF) or interleukin-12 (IL-12). The polynucleotide sequences encoding  
the antigen and the cytokine are under transcriptional control of same or  
different promoter polynucleotide sequences. The expression vector, as a  
DNA vaccine is useful for treating a condition in an organism. The  
present sequence is human herpesvirus 2 complete DNA genome related to



Dd	65305	GACGAGGACGGGGACGAGCGCGAGAGGTTCGCGCGGAGACCGGGGCGCGACGTTGGG	65364
Qy	2095	TACACGGGGGGCCGGTCTCTCGAACCCACCTCCGGGTTTCAAGTCGACACCCGCTGGTGGTG	2154
Dd	65365	TACACGGGGGGCCGGTCTCTCGAACCCACCTCCGGGTTTCAAGTCGACACCCGCTGGTGGTG	65424
Qy	2155	TTTGACTTTGGCAGGCTGTATCCCGAGCATCATTCAGGCCCAACCTGTCTTCAGTACG	2214
Dd	65425	TTTGACTTTGGCAGGCTGTATCCCGAGCATCATTCAGGCCCAACCTGTCTTCAGTACG	65484
Qy	2215	CTCTCCCTCGCGCCCGAGCGGTTCGCGCACTGAGGCGGACCCGGACTACTCTGGAGATC	2274
Dd	65485	CTCTCCCTCGCGCCCGAGCGGTTCGCGCACTGAGGCGGACCCGGACTACTCTGGAGATC	65544
Qy	2275	GAGGTGGGGGGCCGACGGCTGTCTTCTGTGAAGGCCCAACGTACGCGAGAGCTGCTGAGC	2334
Dd	65545	GAGGTGGGGGGCCGACGGCTGTCTTCTGTGAAGGCCCAACGTACGCGAGAGCTGCTGAGC	65604
Qy	2335	ATCTGTCTGCGGACTGTGCTGGCCATGCGAAGCAGATCCGCTCGCGGATCCCCAGAGC	2394
Dd	65605	ATCTGTCTGCGGACTGTGCTGGCCATGCGAAGCAGATCCGCTCGCGGATCCCCAGAGC	65664
Qy	2395	ACCCCGAGGAGCGGCTCTCTCGAACAGCAACAGCGCCGCATCAAGTGTGTGCAAC	2454
Dd	65665	ACCCCGAGGAGCGGCTCTCTCGAACAGCAACAGCGCCGCATCAAGTGTGTGCAAC	65724
Qy	2455	TCGGTGTACGGGTTTACCGGGGCGCAGCAGCGTCTTCTGCGCCCTGCTGCAAGTGTGTGCAAC	2514
Dd	65725	TCGGTGTACGGGTTTACCGGGGCGCAGCAGCGTCTTCTGCGCCCTGCTGCAAGTGTGTGCAAC	65784
Qy	2515	ACCGTGACGACCATCGGCGCGGAGATGCTCTCTCGACGCGCGCGTACGTGCAACGCGCGC	2574
Dd	65785	ACCGTGACGACCATCGGCGCGGAGATGCTCTCTCGACGCGCGCGTACGTGCAACGCGCGC	65844
Qy	2575	TGGGGGAGTTGATCAGCTGCTGGCCGACTTTTCGGAGGCGCGCGCATGCGCGCCCGC	2634
Dd	65845	TGGGGGAGTTGATCAGCTGCTGGCCGACTTTTCGGAGGCGCGCGCATGCGCGCCCGC	65904
Qy	2635	GGTCCGTACTCCATGCGCATCATCTACGGGACACGACTCCATTTTCTGTTTGTGCGCG	2694
Dd	65905	GGTCCGTACTCCATGCGCATCATCTACGGGACACGACTCCATTTTCTGTTTGTGCGCG	65964
Qy	2695	GGCTCAAGCGCGCGGCTGTGGCCATGGGCGACAAAGATGGCGAGCCACATCTCGCGC	2754
Dd	65965	GGCTCAAGCGCGCGGCTGTGGCCATGGGCGACAAAGATGGCGAGCCACATCTCGCGC	66024
Qy	2755	GCGCTGTCTCTCCCGCGATCAAGCTGAGTGCAGAAAGAGTTCAAGCTGCTGCTC	2814
Dd	66025	GCGCTGTCTCTCCCGCGATCAAGCTGAGTGCAGAAAGAGTTCAAGCTGCTGCTC	66084
Qy	2815	ATCGCCAGAAAAAGTACATCGGCGTCACTCGCGGGGCAAGATGCTCATCAAGGCGTG	2874
Dd	66085	ATCGCCAGAAAAAGTACATCGGCGTCACTCGCGGGGCAAGATGCTCATCAAGGCGTG	66144
Qy	2875	GATCTGGTGGCAAAAAACAATGCGGTTTTATCAACCGCACTCCAGGGCCCTGGTTCGAC	2934
Dd	66145	GATCTGGTGGCAAAAAACAATGCGGTTTTATCAACCGCACTCCAGGGCCCTGGTTCGAC	66204
Qy	2935	CTGCTGTTTACGACGATACCGTATCCGAGGCGGCGCGCGTTCAGCGAGCGCCCGCA	2994
Dd	66205	CTGCTGTTTACGACGATACCGTATCCGAGGCGGCGCGCGTTCAGCGAGCGCCCGCA	66264
Qy	2995	GAGGAGTGGCTGGCGGACCCCTGCCCGAGGACTGCGAGGCTTCGGGGCGCTCTCGTA	3054
Dd	66265	GAGGAGTGGCTGGCGGACCCCTGCCCGAGGACTGCGAGGCTTCGGGGCGCTCTCGTA	66324
Qy	3055	GAGCCCATCGGCGCATCACCGACCCCGAGAGGACATCCAGGACTTTGTCTCTCACCGCC	3114
Dd	66325	GAGCCCATCGGCGCATCACCGACCCCGAGAGGACATCCAGGACTTTGTCTCTCACCGCC	66384
Qy	3115	GAATGAGCAGACACCGCGCGGCTTACCAACAGCGCTTGGCCCACTGACGGTGTAT	3174
Dd	66385	GAATGAGCAGACACCGCGCGGCTTACCAACAGCGCTTGGCCCACTGACGGTGTAT	66444
Qy	3175	TACAAGCTCATGGCCCGCGCGAGGTCCCGTCCATCAAGGACCGGATCCCGTACGTG	3234
Dd	66445	TACAAGCTCATGGCCCGCGCGAGGTCCCGTCCATCAAGGACCGGATCCCGTACGTG	66504
Qy	3235	ATCGTGGCCACAGACCCGCGAGGTAGAGAGACGGTTCGCGCGGCTGGCGCCCTCCCGCAG	3294
Dd	66505	ATCGTGGCCACAGACCCGCGAGGTAGAGAGACGGTTCGCGCGGCTGGCGCCCTCCCGCAG	66564
Qy	3295	CTAGACCGCGCGCCCAAGGGAGAGCCCGCCCCCCCCCAGCGGCCCTGCCCCCGGCC	3354
Dd	66565	CTAGACCGCGCGCCCAAGGGAGAGCCCGCCCCCCCCCAGCGGCCCTGCCCCCGGCC	66624
Qy	3355	AAGCGCCCCCGGAGAGCCCGTTCGATGCGGACCCCGCGGAGGCGGTTCGAAGCCCGC	3414
Dd	66625	AAGCGCCCCCGGAGAGCCCGTTCGATGCGGACCCCGCGGAGGCGGTTCGAAGCCCGC	66684
Qy	3415	AAGCTGTGTGTTCGAGCTGGCGGAGGATCCCGGCTACGCCATCGCCCGGGCGGTTCCG	3474
Dd	66685	AAGCTGTGTGTTCGAGCTGGCGGAGGATCCCGGCTACGCCATCGCCCGGGCGGTTCCG	66744
Qy	3475	CTCAACACGGACTATTACTTCTCCACCTGCTGGGGGGCGGCTGCGTGAACGGCC	3534
Dd	66745	CTCAACACGGACTATTACTTCTCCACCTGCTGGGGGGCGGCTGCGTGAACGGCC	66804
Qy	3535	CTGTTTGGAAATAACGCCAAGATCACCGAGAGTCTGTTTAAAGAGGTTTATTTCCGAGAGC	3594
Dd	66805	CTGTTTGGAAATAACGCCAAGATCACCGAGAGTCTGTTTAAAGAGGTTTATTTCCGAGAGC	66864
Qy	3595	TGGCACCCCCCGGACGACGCTGGCGCGCGCTCAAGGCGCGGGTTTCGGGCGCGGGG	3654
Dd	66865	TGGCACCCCCCGGACGACGCTGGCGCGCGCTCAAGGCGCGGGTTTCGGGCGCGGGG	66924
Qy	3655	GCGGCGCTACGCGGAGGAAACTGCTGCGAATGTTGATAGAGCCTTTGATCTTAGCA	3714
Dd	66925	GCGGCGCTACGCGGAGGAAACTGCTGCGAATGTTGATAGAGCCTTTGATCTTAGCA	66984
Qy	3715	TGA 3717	
Dd	66985	TGA 66987	
RESULT 6			
AAD30079			
ID	AAD30079 standard; DNA; 3708 BP.		
XX	AAD30079;		
DT	17-MAY-2002 (first entry)		
XX	Herpes simplex virus (HSV1-KOS-M1) mutant DNA polymerase gene.		
XX	Herpes virus; medicinal; therapy; binding domain; DNA polymerase gene;		
KW	antiviral; enzyme; mutant; ds.		
XX	Herpes simplex virus.		
OS			
XX			
FT	Key	Location/Qualifiers	
CDS		1..3708	
FT	/*tag= a		
FT	/product= "Mutant DNA polymerase"		
XX	WO200206513-A2.		
PN			
XX			
PD	24-JAN-2002.		
XX			
PF	13-JUL-2001; 2001WO-US016525.		
XX			
PR	13-JUL-2000; 2000US-0218118P.		
PR	13-APR-2001; 2001US-0283880P.		
XX			
PA	( PHAA ) PHARMACIA & UPJOHN CO.		
XX			



QY 1621 CTGAACGCGCTGCGCGAGCGCTCTTTGAAGGACAAAGAAAGGATCTGAGCTACCGGAC 1680  
DB 1618 CTCACGCGCTGCGCGAAGCGCTCTGAAGGACAAAGAAAGGACCTGAGCTATCGGAC 1677  
QY 1681 ATCCCGCCTACTAGCGCTCCGGGCCCGCGCAGCGCGGGGTGATCGGGAGTATTGTGTG 1740  
DB 1678 ATCCCGCCTACTAGCGCGCGCGCGCGCGAAGCGGGGTGATCGGGGAGTACTGCATA 1737  
QY 1741 CAGGACTCGCTGCTGCTGCTGCGGCGAGCTGTTCTTCAAGTTTCTGCGCGACCTCGAGCTTCC 1800  
DB 1738 CAGGATTCCTGCTGCTGCTGCGGCGAGCTGTTTAAAGTTTTCGCCCATCTGAGAGCTCTG 1797  
QY 1801 GCGTTCGCGCGCTGCGCGGCGATCAACATCACCGCCACCATCTACGACGCGCAGAGATC 1860  
DB 1798 GCGGTCGCGCGCTTGGCGGGTATTAAATCATCACCGCCACCATCTACGACGCGCAGAGATC 1857  
QY 1861 GCGGTCCTCAGTTCCTGCTGCGGCTTGGCGGCGCAGAGGCTTTCATCTGCGGACACC 1920  
DB 1858 GCGGTCCTTACGCTGCTGCTGCGGCTTGGCGGCGCAGAGAGGCTTATTCTGCGCGGACACC 1917  
QY 1921 CAGGGGCGGTTTTCGGGGCTTCGACAAAGAGGCGGCCAAAGCGCGCGCGCTGCTCGGGG 1980  
DB 1918 CAGGGGCGATTAGGGGCGCGGGGGGAGGCGGCCAAGCGTTCGGCGCGACCGCGGAG 1977  
QY 1981 GAAGGGAGCGCGCGGGGACCGGAAACGGGACGAGGATAGGACGACGAGGACGAG 2040  
DB 1978 GACGAGGAGCGCGCAGAGGAGGAGGGGAGGAGC-----AGGACGACGCGAGGAGGC 2031  
QY 2041 GACGGGACGAGCGGAGGAGGCTCGCGGCGAGACCGGGGCGCGGACGTTGGGTACGAG 2100  
DB 2032 GGGGCGGAGCGCGGAGCGCGAGGCGCGCGGAGACCGCGCGCGCGGACGCTGGGGTACCG 2091  
QY 2101 GGGGCGCGGGTCTCGACCCCACTCCGGGTTTACGTCGACCCCGCTGGTGGTCTTTGAC 2160  
DB 2092 GGGGCGAGGTCCTTGACCCCACTTCGGGGTTTACGTGAACCCCGCTGGTGGTCTTCAC 2151  
QY 2161 TTTGCCAGCTGTATCCCGAGCATCATCCAGGCCCAACACTGTGCTTTCAGTACGCTCTCC 2220  
DB 2152 TTTGCCAGCTGTATCCCGAGCATCATCCAGGCCCAACACTGTGCTTTCAGTACGCTCTCC 2211  
QY 2221 CTGCGGCGCGAGCGCTCGCGACCTTGAGGCGGACCGGGATCTACTGAGATCGAGGTG 2280  
DB 2212 CTGAGGGCGGACGCGAGTGGCGACCTTGAGGCGGGCAAGGACTACTCTGAGATCGAGGTG 2271  
QY 2281 GGGGCGCGAGCGCTGTTCTTCTGTAAGGCCCACTAGCGAGAGCTGCTGAGCATCTTG 2340  
DB 2272 GGGGCGGACGCGCTGTTCTTCTGTAAGGCTCAGCTGCGAGAGAGCTCTCTCAGCATCTC 2331  
QY 2341 CTGCGCGATGGCTGGCCATGCGAAGCAGATCCGCTCGCGGATCCCGGAGCAGACCCCC 2400  
DB 2332 CTGCGGACCTGGCTCGCATGCGAAGCAGATCCGCTCGCGGATTCGCCAGAGCAGCCCC 2391  
QY 2401 GAGAGGCGCTCTCTCGACAGCAAGCGCGCGCATCAAGGTGGTGTGCAACTCGGTG 2460  
DB 2392 GAGAGGCGCTGCTCTCTGGAACAGCAGCAGGCGCGCCATCAAGGTGCTGTGTAATCGGTG 2451  
QY 2461 TACGGGTTACCGGGGCGACGACGCTTCTGCTCCCTGCTGACAGTGGCGCGCCACCGGTG 2520  
DB 2452 TACGGGTTACGGAGGCGACGAGCTCTGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2511  
QY 2521 ACACCATGCGCGCGAGATGCTCTCTCGCGACGCGCGGTACGTGACGCGCGCTGGGCG 2580  
DB 2512 ACACCATGCGCGCGAGATGCTCTCTCGCGACGCGCGGTACGTGACGCGCGCTGGGCG 2571  
QY 2581 GAGTTCAGTCTGCTGGCGCATTTTCGGAGGCGCGCGCATGCGGCGCGCGCGCTCG 2640  
DB 2572 GCTTTCGAACAGCTCTTGGCGGATTTCCGGAGGCGCGCGCATGCGGCGCGCGCGCG 2631  
QY 2641 TACTCCATGCGCATCATCTACGGGACACGAGCTTCATTTTCTGTTTGTGCGCGGCTC 2700  
DB 2632 TATTCCATGCGCATCATCTACGGGACACGAGCTTCATATTGTTGCTGTGCGCGGCTC 2691  
QY 2701 ACGGCGCGGGCTTGGTGGCCATGGCGGACAAAGATGGCGGACCATCTCGCGCGCGCTG 2760

DB 2692 ACGGCGCGCGGCTGACGGCGCATGGCGGACAAAGATGGCGGACCATCTCGCGCGCGCTG 2751  
QY 2761 TTTCTCTCCCGCATCAAGCTCGAGTCGAAAAAAGTTTCCAAAGAGTGTCTCATCGCC 2820  
DB 2752 TTTCTGCGCGCGCATCAAACTCGAGTGCAGAAAGAGCTTCAACAGCTGTCTCATCGCC 2811  
QY 2821 AAGAAAAAGTACATCGCGCTCATCTCGGGGGCAAGATGCTCATCAAGGGGCTGTGATCTG 2880  
DB 2812 AAGAAAAAGTACATCGCGCTCATCTCGGGGGTAAAGATGCTCATCAAGGGGCTGTGATCTG 2871  
QY 2881 GTGCGCAAAAAAATCTCGGCTTTTCAACCGCACCTCTCAGGGCCCTGGTCCGACTGCTG 2940  
DB 2872 GTGCGCAAAAAAATCTCGGCTTTTCAACCGCACCTCTCAGGGCCCTGGTCCGACTGCTG 2931  
QY 2941 TTTTACGACGATACCGCTATCCGAGCGCGCGCGGCTTAGCGAGCGCGCGCGAGAG 3000  
DB 2932 TTTTACGACGATACCGCTATCCGAGCGCGCGCGCGCTTAGCGAGCGCGCGCGAGAG 2991  
QY 3001 TGGCTGGCGGACCCCTGCGCGAGGAGTGCAGGCTTTCGGGGCGCTCTCTGTAGACGCC 3060  
DB 2992 TGGCTGGCGGACCCCTGCGCGAGGAGTGCAGGCTTTCGGGGCGCTCTCTGTAGACGCC 3051  
QY 3061 CATCGCGCATACCGACCCCGAGAGGAGCATCCAGGACTTTTGTCTTCCACCGCGCAACTG 3120  
DB 3052 CATCGCGCATACCGACCCCGAGAGGAGCATCCAGGACTTTTGTCTTCCACCGCGCAACTG 3111  
QY 3121 AGCAGACACCGCGCGGTACACCAAGAGGCTTGGCGGCTTGGCGGCTTGTATTAAG 3180  
DB 3112 AGCAGACACCGCGCGGTACACCAAGAGGCTTGGCGGCTTGGCGGCTTGTATTAAG 3171  
QY 3181 CTATGCGCGCGCGCGGAGTCCGCTCATCAAGGACCGGATCCCGTACGTAGCTGCTG 3240  
DB 3172 CTATGCGCGCGCGCGGAGTCCGCTCATCAAGGACCGGATCCCGTACGTAGCTGCTG 3231  
QY 3241 GCCCAGACCCCGCGAGGTAGAGGAGACGCTCGCGGCTTGGCGGCTTCCCGGAGCTAGAC 3300  
DB 3232 GCCCAGACCCCGCGAGGTAGAGGAGACGCTCGCGGCTTGGCGGCTTCCCGGAGCTAGAC 3291  
QY 3301 GCCCGCGCGCGAGGAGCGAGCGCGCGCGCGCGCGCGCTTCCCGGCGCGCGCGCGCG 3360  
DB 3292 GCCCGCGCGCGAGGAGCGAGCGCGCGCGCGCGCGCGCTTCCCGGCGCGCGCGCGCG 3351  
QY 3361 CCCCGGAGACCGCGCTCGCATGCGACCCCGCGGAGCGGCTCCAAAGCCCGCAAGCTG 3420  
DB 3352 CCCCGGAGACCGCGCTCGCATGCGACCCCGCGGAGCGGCTCCAAAGCCCGCGAGCTG 3411  
QY 3421 CTGCTGTCCGAGCTGGCGGAGTCCCGGGTACGCGCATCGCGCGCGGCGCTTCCGCTCAAC 3480  
DB 3412 CTGCTGTCCGAGCTGGCGGAGTCCCGCATAGCGCATTTGCCACGCGCTCGCTGAAC 3471  
QY 3481 ACGGACTATTACTTCTGCGACCTGCTGGGGCGCGCTGCGTGAAGTTCAAGGCCCTGTTT 3540  
DB 3472 ACGGACTATTACTTCTCCACCTGTTGGGGCGCGCTGCGTGAATTTCAAGGCCCTGTTT 3531  
QY 3541 GGAATAACCCCAAGATCACCGAGAGTCTGTTAAAGAGTTTATTCCCGAGAGCTGGCAC 3600  
DB 3532 GGAATAACCCCAAGATCACCGAGAGTCTGTTAAAGAGTTTATTCCCGAGAGTGGCAC 3591  
QY 3601 CCCCGGAGACGCTGGCGCGCGCTCAGGGCGCGCGGGGTTTCGGCGCGCGGGGCGCGCG 3660  
DB 3592 CCCCGGAGACGCTGGCGCGCGCGCTCAGGGCGCGCGGGTTCGGGGCGGTGGGTGCGCGCG 3651  
QY 3661 GCTACGGCGGAGGAACTCTCGAATGTTGATAGAGCTTTGATCTACTAGCATGA 3717  
DB 3652 GCTACGGCGGAGGAACTCTCGAATGTTGATAGAGCTTTGATCTACTAGCATGA 3708

RESULT 7  
AAD30080  
ID AAD30080 standard; DNA; 3708 BP.  
XX  
AC AAD30080;



XX DT 17-MAY-2002 (first entry)  
 XX DE Herpes simplex virus (HSV1-F-M1) mutant DNA polymerase gene.  
 XX KW Herpes virus; medicinal; therapy; binding domain; DNA polymerase gene;  
 XX KW antiviral; enzyme; mutant; ds.  
 XX OS Herpes simplex virus.  
 XX FH Key Location/Qualifiers  
 FT CDS 1..3708  
 FT /\*tag= a  
 FT /product= "Mutant DNA polymerase"  
 XX W0200206513-A2.  
 XX PN 24-JAN-2002.  
 XX XX 13-JUL-2001; 2001WO-US016525.  
 XX PF 13-JUL-2000; 2000US-0218118P.  
 XX PR 13-APR-2001; 2001US-0283880P.  
 XX XX (PHAA ) PHARMACIA & UPJOHN CO.  
 XX PA Homa PL, Wathen MW, Hopkins TA, Thomsen DR;  
 PI WPI; 2002-179800/23.  
 XX DR P-PSDB; AAE18856.  
 XX DR  
 XX PT Selecting compounds that inhibit herpes viruses by comparing inhibitory  
 PT concentration of a compound of interest that inhibits wild-type herpes  
 PT virus and domain mutant herpes virus, and selecting compound of interest.  
 XX PS Claim 25; Fig 5; 126pp; English.  
 XX CC The present invention relates to a method for selecting compounds that  
 CC inhibit herpes viruses. The method involves measuring IC 5.0 of compound  
 CC of interest that inhibits wild-type herpes virus and domain mutant herpes  
 CC virus mutant herpes virus which is the same strain as wild-type herpes  
 CC virus, comparing IC 5.0 of the compound inhibiting wild-type herpes virus  
 CC with IC 5.0 of the compound inhibiting mutant herpes virus and selecting  
 CC the compound, where IC 5.0 of the compound of interest that inhibits  
 CC mutant herpes virus is at least 3 times greater than IC 5.0 of the  
 CC compound that inhibits wild-type herpes virus. The method is useful for  
 CC selecting compounds that inhibit herpes viruses. The compound is useful  
 CC for manufacture of medicinals for selectively treating diseases caused by  
 CC herpes viruses such as herpes viral infection, or for selectively  
 CC inhibiting herpes viruses, in a human host by administering a compound to  
 CC human in need of such treatment, where the compound inhibits herpes  
 CC viruses by interaction with the binding domain in the viral DNA  
 CC polymerase, and IC 5.0 of the compound that inhibits a binding domain  
 CC mutant herpes virus is at least 3 times, preferably 5 times greater than  
 CC IC 5.0 of the compound that inhibits the wild-type herpes virus which is  
 CC the same strain as the mutant herpes virus. The present sequence is  
 CC Herpes simplex virus (HSV1-F-M1) mutant DNA polymerase gene  
 XX  
 SQ Sequence 3708 BP; 659 A; 1237 G; 1201 G; 611 T; 0 U; 0 Other;  
 Query Match 82.1%; Score 3053.4; DB 6; Length 3708;  
 Best Local Similarity 89.2%; Pred. No. 0;  
 Matches 3317; Conservative 0; Mismatches 391; Indels 9; Gaps 2;  
 Qy 1 ATGTTTTCGCGGGGGGGCCGACCTTCCCGGGGGGAGTCTCGGGCTCGGGCGCG 60  
 Db 1 ATGTTTTCGCGGGGGGGGGCGCTGTCTCCCGGAGGAAAGTCTCGGGCGCGGGCG 60  
 Qy 61 TCTGGTTTTCGCGGG 120  
 Db 61 TCCGGGTTTTCGCGGG 117  
 Qy 121 CGCGCGGAGAACTTCTTAAACCCCAACCTCTCGCTCAGACCGGAGCGACGCAAGGGCCCC 180

Db 118 TTGAGGCAAACTTTTACAAACCCCTACTCTCGCCCACTCGAGTCGGAGCGAAGAGCCGACC 177  
 Qy 181 GGGCGGGCTCAGCGCCATAGCTACTACAGGAGTGCAGCGAATTTTCGATTTATCGCCCGC 240  
 Db 178 GGGCCAAACAGCGCCATAGCTACTATAGCGAATGCGATGAATTCGATTTCATCGCCCGC 237  
 Qy 241 CGTTTCGTCGAGGAGCGCCCGGGGAGCGCACCGGGGTCCACGACGCGCGCTC 300  
 Db 238 CGGGTCTGAGCAGGATGCCCGCCGAGAGCGCGCGGGGTGCAACGCGTCACTC 297  
 Qy 301 CGGCGCGCCCTAAGGTGTACTGCGGGGGGAGCGAGCGGACGCTCTCTCCCGTGGGGCGC 360  
 Db 298 AAGCGCGCCCAAGGTGTACTGCGGGGGGAGCGAGCGGACGCTCTCTCCCGTGGGGTCG 357  
 Qy 361 GAGGGCTTCGCGCGCGGTCTGCGCTGCGGGGGGTGCGGACCATGCCCCCAAGGGG 420  
 Db 358 GCGGGTTCGCGCGCGGGCGCTCGCGCTGTGGGGGGCGGTGGACCAAGCGCCCGGGGG 417  
 Qy 421 TTCGACCCCAACCGTCAACCGTCTTCCAGCTGTACGACATCTCTGGAGCAGCTGGGAACGCG 480  
 Db 418 TTCAAACCCACCGTCAACCGTCTTTCACGTGTACGACATCTCTGGAGAACGTGGAGCAGCG 477  
 Qy 481 TACAGCATGCGCGCGCCAGCTCAGCGAGCTTTATGAGCGGATTCAGCGCGCGCGCG 540  
 Db 478 TACGGCATGCGCGCGCGCCAGTTCACGCGCGGTTCATGAGCGCCATCACACGACGCGG 537  
 Qy 541 ACGTCACTACCGTCTCTGGGTCTGACCCCGAAGGCATCGCTCGCGCTTACGCTAC 600  
 Db 538 ACCGTCACTACCGTCTCTGGGCTGACTTCGGAAGGCCACCGGGTGGCGGTTCACGTTTAC 597  
 Qy 601 GGCACGCGGAGTACTTTTACATGAACAAGCGGAGTGGATCGGACCTTGCAGTGCCT 660  
 Db 598 GGCACGCGGAGTACTTTTACATGAACAAGAGGAGGTTCGACAGGACCTTACAATGCGC 657  
 Qy 661 GCGCGCGCGATCTCTCGAGCGCTGCGCGCGCGCTGCGGAGTCTCGCGGGGGCGTCG 720  
 Db 658 GCGCCACGAGATCTCTCGAGCGCATGCGCGCGCGCTGCGGAGTCTCGCGGGGGCGTCG 717  
 Qy 721 TTCGCGGATCTCTCGGAGCACCTTTCGAGGCGGAGTGTGGAGCGCGCGCTGCTAC 780  
 Db 718 TTCGCGGATCTCTCGGAGCACCTTTCGAGGCGGAGTGTGGAGCGCACCGAGCTGCTAC 777  
 Qy 781 TATTACGAAACGCGCGCGACCTTACTACCGGTCTTCTGCGAAGCGGGGGCGCGCTG 840  
 Db 778 TACTACGAGACGCGCGCGCTCTGTGTTTACCGGTCTTACGCTCCGAGCGGGCGCTGCTG 837  
 Qy 841 GCCTACTGTGCGACAACTTTTTCGCGCGCATCAGGAAGTACGAGGGGGGGCGTGCAGCC 900  
 Db 838 TCGTACTGTGCGACAACTTCTCGCGCGCATCAAGAAAGTACGAGGGGTGGGGTGCAGCC 897  
 Qy 901 ACCACCGGTTTATCTTGGACAAACCGGGGTGTGTACCTTCGCTCGGTACCGCTCAAG 960  
 Db 898 ACCACCGGTTTATCTTGGACAAACCGGGGTGTGTACCTTCGCTCGGTACCGCTCAAG 957  
 Qy 961 CCGCGCGCGGGAACGCGCGCGCGCAACCGCGCGCGCGCGCGGTTCGGAACCTCGAGC 1020  
 Db 958 CCGCGCGGAACAACACGCTAGCCGCGCGCGCGCGCGGTTCGGAACCTCGAGC 1017  
 Qy 1021 GAGTCTGAGTTTAACTGACGCGGGAACCTCGCGTTCGAGGGGGGGCGATGTGTGACTG 1080  
 Db 1018 GAGTCTGAGTTTAACTGACGCGGGAACCTCGCGCATTCGAGGGGGGGCGATGAGCGACTA 1077  
 Qy 1081 CCGGCTTACAGCTCATGTCTTCGATATCGAATGCAAGCGCGGGGGGGAGGACGAGCTG 1140  
 Db 1078 CCGGCTATCAAGCTCATGTCTTCGATATCGAATGCAAGCGCGGGGGGGAGGACGAGCTG 1137  
 Qy 1141 GCCTTTCCGCTCGGGAACCGCGCGGAAGACTCTGTCATTCAGATCTCTGTCTCTCTAC 1200  
 Db 1138 GCCTTTCCGCTCGGCGGCAACCGCGAGGACCTGTGTCATTCAGATATCTGTCTCTCTAC 1197  
 Qy 1201 GAGCTGTCACCAACCGCGCTCGAGCATCTCTCTGTTTTCGCTCGGATCTCTGCGACCTC 1260



Db 1198 GACCTGTCCACACCGCCCTGGAGCAGCTCTCTCTGTTTTCGCTCGGTTCTTGGACCTC 1257  
Qy 1261 CCCGAGTCCCACTCAGGATCTCGCTCCAGGGGSCCTCGCGCCCGCTGCTCTGGAG 1320  
Db 1258 CCCGATCCCACTGACGAGTGGCGCCAGGGSCCTGCCACGCCCGTGGTCTGGAA 1317  
Qy 1321 TTGTGACGGAATTCGAGATCTGCTGGCTTTCATGACCTTTCGTAAGCAGTACGGCCCC 1380  
Db 1318 TTGACACGGAATTCGAGATCTGTTGGCTTTCATGACCTTTCGTAAGCAGTACGGCCCC 1377  
Qy 1381 GAGTTCGTGACGGGTGACAAATCATCACTTCACTTCACTTGGCTTTCGCTGACCAAGCTG 1440  
Db 1378 GAGTTCGTGACGGGTGACAAATCATCACTTTCGACTTGGCTTTCGCTGACCAAGCTG 1437  
Qy 1441 ACGGAGATCTCAAGGTCCCGCTCGA CCGGTGACGGGCGCATGAACGGCGGGGTGTTTC 1500  
Db 1438 ACGGATCTTCAAGGTCCCGCTCGA CCGGTGACGGGCGCATGAACGGCGGGGTGTTTC 1497  
Qy 1501 CGGTGTGGGACATCGGCGACAGGCACTTTTCAAGGCGCAGCAAGATCAAGGTGAACGGG 1560  
Db 1498 CGGTGTGGGACATAGGCGACAGGCACTTTTCAAGGCGCAGCAAGATCAAGGTGAACGGG 1557  
Qy 1561 ATGCTGAACATCGACATGATCGGATCATCAAGGCGCAGCAAGGTGAACGTGACGCTACAG 1620  
Db 1558 ATGCTGAACATCGACATGATCGGATTAATACCGCAAGATCAAGCTTCGAGCTACAG 1617  
Qy 1621 CTGAACGCGCTCGCGAGGCGCTTGAAGGACAGGAGGATCTGAGCTACCGGAC 1680  
Db 1618 CTGAACGCGCTCGCGAGGCGCTTGAAGGACAGGAGGATCTGAGCTACCGGAC 1677  
Qy 1681 ATCCCGCTACTACGCTCCGCGCCGCGCAGGCGCGGGTGATCGGCGAGTATGTGTG 1740  
Db 1678 ATCCCGCTACTACGCGCGCGCGCGCAACCGCGGGTGATCGGCGAGTATGCGATA 1737  
Qy 1741 CAGGATCTGCTGCTCGGCGAGCTGTTCTTCAAGTTCGCGCGACCTGAGGCTTTC 1800  
Db 1738 CAGGATCTGCTGCTGCTGCGGCGAGCTGTTTAAAGTTCGCGCGACCTGAGGCTCTCG 1797  
Qy 1801 GCCGTGCGGCTCGGCGGCGCATCAATCAACCGCGCACCATCTACGACGCGCAGCATC 1860  
Db 1798 GCCGTGCGGCTCGGCGGCGGATTAATCAATCCCGCACCATCTACGACGCGCAGCATC 1857  
Qy 1861 CGGCTCTTACGCTGCTCTGCGCTTTCGCGCGCAGAGGCTTTCATCTGCGCGACAC 1920  
Db 1858 CGGCTCTTACGCTGCTGCTGCGCTGCGCGACAGAGGCTTTCATCTGCGCGACAC 1917  
Qy 1921 CAGGGCGGTTTCGCGGCTCGA CAGGAGCGCGCCAAAGCGCGCGCTGCTCGGGGG 1980  
Db 1918 CAGGGCGGATTTAGGGGCGCGGGGGGAGGCGCCAAAGCGCTCCGCGCGCAGCGCGGGAG 1977  
Qy 1981 GAAGGGAGCGGCGGGGACGGAAACGGGGACGAGGATAGGACGACGACGAGGAG 2040  
Db 1978 GACGAGAGCGGCCAGAGGAGGAGGAGGAGCG-----AGGACGACGAGGAGGGC 2031  
Qy 2041 GACGGGACGAGCGCGAGGAGGTTCGCGCGAGACCGGGGCGCGGCGACGTTGGGTACAG 2100  
Db 2032 GGGGCGAGCGGAGCGCGAGGCGCGCGGAGACCGCGCGCGCGGCGGAGTACAG 2091  
Qy 2101 GGGGCGGCTCTCGACCCACCTCTCGGGTTTCAGCTCGACCCCGTGGTGGTTCGAG 2160  
Db 2092 GGGGCGAGGCTCTTGAACCCACCTTCGGGGTTTCATGTGAACCCCGTGGTGGTTCGAC 2151  
Qy 2161 TTTCCAGGCTGTATCCCGAGCATCATCAGGCCACACCTGTGCTTCAGTACGCTCTCC 2220  
Db 2152 TTTCCAGGCTGTATCCCGAGCATCATCAGGCCACACCTGTGCTTCAGCAGCTCTCC 2211  
Qy 2221 CTGCGGCCGAGGCGCTCGCGACCTTGAAGCGGACCGGGACTACCTGAGATCGAGGTG 2280  
Db 2212 CTGAGGGCGAGCGAGTGGCGACCTTGAAGCGGCGGCGAGGACTACCTTGGAGATCGAGGTG 2271  
Qy 2281 GGGGCGGAGCGGCTGTTCTTCTGTAAGGCGCACGTA CCGGAGGCGCTGCTGAGCATCTG 2340  
Db 2272 GGGGCGGAGCGGCTGTTCTTCTGTAAGGCGCACGTA CCGGAGGCGCTGCTGAGCATCTG 2331

Qy 2341 CTGCGCGACTGCTGGCTGGCAAGCAGATCCGCTCGCGGATCCCGCAGAGCACCC 2400  
Db 2332 CTGCGGGAATCGCTCGCATTCGAAAGCAGATCCGCTCGCGATTCGCCAGAGCACCC 2391  
Qy 2401 GAGGAGCGCTCTCTCGACAAAGCAACAGCGCCCGCATCAAGGTGGTGTGCAACTCGGTG 2460  
Db 2392 GAGGAGCGCTGCTCTCTGGACAAAGCAGCGCCCGCATCAAGGTGCTGTGTAATCTCGGT 2451  
Qy 2461 TACGGGTTACCGGGGCGACGACGCTTCTGCGCTGCTGCGCTGCGAGCGCGCCCGCTG 2520  
Db 2452 TACGGGTTACCGGAGCGACGACGCTTCTGCGCTGCTGCGCTGCGAGCGCGGTG 2511  
Qy 2521 ACAGACATCGCGCCCGAGATGCTCTCGCGACGCGCGGTACGTGCGCGCTGGGCG 2580  
Db 2512 ACAGACATCGCGCCCGAGATGCTCTCGCGACCGCGCGGTACGTGCGCGCTGGGCG 2571  
Qy 2581 GAGTTCAGTCTGCTGGCGACTTTCCGAGGCGCGCGCATGCGCGCCCGCGCTCG 2640  
Db 2572 GCCTTCGAAACAGCTCTCTGGCGATTTCCCGAGGCGCGCGACATGCGCGCCCGCGGCCC 2631  
Qy 2641 TACTCCATGCGCATCATCTACGGGACACGCGACTCCATTTTCGTTTGTGCGCGGCTC 2700  
Db 2632 TATTCCATGCGCATCATCTACGGGACACGCGACTCCATCTTGTGTGCTGCGCGGCTC 2691  
Qy 2701 ACGCGCGCGCTGCTGGCGCATGCGCGACAAAGATGCGAGCGCACATCTCGCGCGCTG 2760  
Db 2692 ACGCGCGCGCTGCGCGCATGCGCGCGACAAAGATGCGAGCGCACATCTCGCGCGCTG 2751  
Qy 2761 TTCTCTCCCGCATCAAGCTCGAGTGGGAAAAACGTTTCAACAAAGCTGCTCTCATCGCC 2820  
Db 2752 TTTCTGCTCCCGCATCAAGCTCGAGTGGGAAAAAGCTTCAACAAAGCTGCTCTCATCGCC 2811  
Qy 2821 AAGAAAAATACATCGCGCTCATCTCGGGGCGAAGATGCTCATCAAGGGCGTGGATCTG 2880  
Db 2812 AAGAAAAATACATCGCGCTCATCTACGGGGTGAAGATGCTCATCAAGGGCGTGGATCTG 2871  
Qy 2881 GTGCGGAAAAACATCGCGGTTTATCAACCGCACCTCCAGGGCCCTGGTGACCTGCTG 2940  
Db 2872 GTGCGGAAAAACATCGCGGTTTATCAACCGCACCTCCAGGGCCCTGGTGACCTGCTG 2931  
Qy 2941 TTTTACGACATACCTATCCGAGCGCGCGCTTAGCGAGCGCGCGCGAGAGGAG 3000  
Db 2932 TTTTACGACATACCTATCCGAGCGCGCGCTTAGCGAGCGCGCGCGAGAGGAG 2991  
Qy 3001 TGGTGGCGGACCCCTGCGCGAGGAGCTGAGGCGTTTGGGGCGCTCTGCTGAGACGCC 3060  
Db 2992 TGGTGGCGGACCCCTGCGCGAGGAGCTGAGGCGTTTGGGGCGCTCTGCTGAGACGCC 3051  
Qy 3061 CATCGGCGCATCACCGACCGGAGGAGCATCCAGGACTTGTCTCACCGCGCGAACTG 3120  
Db 3052 CATCGGCGCATCACCGACCGGAGGAGCATCCAGGACTTGTCTCACCGCGCGAACTG 3111  
Qy 3121 AGCAGACACCGCGCGCTACACAAACAGCGCTGCGCGCACCTGACGGTGTATTACAAG 3180  
Db 3112 AGCAGACACCGCGCGCTACACAAACAGCGCTGCGCGCACCTGACGGTGTATTACAAG 3171  
Qy 3181 CTATGGCCCGCGCGAGGTTCCCGTCATCAAGGACCGGATCCCGTACGTGATCGTG 3240  
Db 3172 CTATGGCCCGCGCGAGGTTCCCGTCATCAAGGACCGGATCCCGTACGTGATCGTG 3231  
Qy 3241 GCCCAGACCGCGAGGTAGAGGAGAGCGTTCGCGGCTGGCGCGCTCCCGGAGCTGAC 3300  
Db 3232 GCCCAGACCGCGAGGTAGAGGAGAGCGTTCGCGGCTGGCGCGCTCCCGGAGCTGAC 3291  
Qy 3301 GCCCGCGCCCGAGGAGCGAGCGCGCGCGCGCGCTGCGCTCCCGGCGCAAGCGC 3360  
Db 3292 GCCCGCGCCCGAGGAGCGAGCGCGCGCGCGCGCTGCGCTCCCGGCGCAAGCGC 3351  
Qy 3361 CCCCGGAGACCGCTGCGATGCGAGCGCGCGCGCGCGCGCTGCGCTCCCGGCGCAAGCGC 3420  
Db 3352 CCCCGGAGACCGCTGCGATGCGAGCGCGCGCGCGCGCGCTGCGCTCCCGGCGCAAGCGC 3411



Qy	841	GCCTACCTGTGCGCAACATTTTGGCCCGCGCATCAGGAAGTACGAGGGGGCGTTCGACGCC	900
Db	838	TCGTACCTGTGCGCAACATTTCTGCCCGCGCATCAAGAAAGTACGAGGGTGGGGTTCGACGCC	897
Qy	901	ACCAACCGGTTTATCTCTGGACAACCCCGGGGTTTGTTCACCTTCGGCTGGTACC GCCCTCAAG	960
Db	898	ACCAACCGGTTTATCTCTGGACAACCCCGGGTTCGTTCACCTTCGGCTGGTACC GTTCTCAAA	957
Qy	961	CCCGCCCGGGGAACGCGCGCGGCCAACACGCGGCCCCCGCAGCGGTTTCGGAACCTTCGAGC	1020
Db	958	CCGGCCCGGAACAACACGCTAGCCAGCCGCGGGCCCGGATGGCTTCGGGGAATCCAGC	1017
Qy	1021	GACGTGAGTTTAACCTGCAACCGGCGGCAACCTGGCCGCTCCAGGGGGCCATGTGTGACCTG	1080
Db	1018	GATGTGAGTTTAACTGTACGGCGGGAACAACCTTGCCCATGAGGGGGGCATGAGCGACCTA	1077
Qy	1081	CCGGCCCTAACAGCTCATGTCTTCGATATCGAATGCAAGGCCCGGGGGGAGGACGAGCTG	1140
Db	1078	CCGGCATAAAGCTCATGTCTTCGATATCGAATGCAAGCGGGGGGGAGGAGCGAGCTG	1137
Qy	1141	GCCTTTCCGGTTCGCGGAACCCCGGAAGACCTCGTCAATCCAGATCTCTCTGTCTGTACTAC	1200
Db	1138	GCCTTTCCGGTTCGCGGCACCCCGGAGAACCTTGCTCATCCAGATATCTCTGTCTGTACTAC	1197
Qy	1201	GACCTGTCCACACCGCCCTCGAGCACAATCTCTGTGTTTTCGCTCGGATCTCTCGGACCTC	1260
Db	1198	GACCTGTCCACACCGCCCTCGAGACAGCTCTCTCTGTGTTTTCGCTCGGTTCTCTCGGACCTC	1257
Qy	1261	CCGAGTCCCAACCTCAGCGATCTCGCTCCAGGGGCTCGCGGCCCGCTCGTCCTGGAG	1320
Db	1258	CCGAATCCCAACCTGAAAGAGCTGCGGGCCAGGGGCTGCCCCACGCCCGGTTCGGA	1317
Qy	1321	TTTGACAGCGAAATTCGAGATGCTGTGGCCCTTCATGACCTTCGTCAAGCAGTACGGCCCC	1380
Db	1318	TTGACAGCGAAATTCGAGATGCTGTGGCCCTTCATGACCTTCGTGAAACAGTACGGCCCC	1377
Qy	1381	GAGTTCTGACCGGGTACAAATCATCAATCAACTTCGACTGGCCCTTCGTCTGACCAAGCTG	1440
Db	1378	GAGTTCTGACCGGGTACAAATCAATCAACTTCGACTGGCCCTTCGTCTGACCAAGCTG	1437
Qy	1441	ACGGAGATCTCAAGGTCCGCTCGACGGGTACGGGGCATGAACGGCGGGGTGTTC	1500
Db	1438	ACGGACATTTACAGGTTCGCCCTTGAGCGGTAACGGCCGATGAACGGCCGGGGGTGTTC	1497
Qy	1501	CGGTGTGGGACATCGGCCAGAGCCACTTTGAGAAGCGAGCAAGATCAAGGTGAACGGG	1560
Db	1498	CGGTGTGGGACATAGGCCAGAGCCACTTCAGAGGGCAGCAAGATTAAGGTGAACGGC	1557
Qy	1561	ATGGTGAACATCGACATGTACGGATCATCACCGACAAGGTCAAACTCTCCAGCTACAAG	1620
Db	1558	ATGGTGAACATCGACATGTACGGATCATTAACCGACAAGATCAAGCTCTCGAGCTACAAG	1617
Qy	1621	CTGACGCGCTCGCGAGCGGTCTTGAAAGGCAAGAGAGGATCTGAGCTACCGGAC	1680
Db	1618	CTCAACGCGGTGGCCGAAGCGTCTTGAAAGGCAAGAGAGGACCTGAGCTATCGGAC	1677
Qy	1681	ATCCCCGCTTACAGCTCTCGGGCCCGCGACGCGGGGTGATCGCGAGTATTGTGTG	1740
Db	1678	ATCCCCGCTTACAGCTCTCGGGCCCGCGACGCGGGGTGATCGCGAGTACTGCATA	1737
Qy	1741	CAGGACTCGTGTGCGGCAAGCTGTTCTTCAAGTTTCTGCGCACCTTGGAGCTTTCC	1800
Db	1738	CAGGATTCCTGTGTGGTGGCCAGCTGTTTTTAAAGTTTTTGGCCCATCTGGAGCTCTCG	1797
Qy	1801	GCGTTCGCGGCTTGGCGGCGATCAACATCACCGGACCAATCTACAGCGCCGACGATC	1860
Db	1798	GCGTTCGCGGCTTGGCGGCGATTAACATCACCGGACCAATCTACAGCGCCGACGATC	1857
Qy	1861	CGGCTCTTACGTCCTCTCGCTTGCGGGCCAGAGGGCTTTCATCTCTGCGGACACC	1920
Db	1858	CGGCTCTTACGTCCTCTGCGCTTGCGGCGACGACGAGGGCTTTCATCTCTGCGGACACC	1917
Qy	1921	CAGGGGCGGTTTCGGGGCTTCGACAAGGAGGGGCCCAAGCGCCCGCGCTGCTCTCGGGG	1980

Db 2992 TGGCTGGCGGACCCCTGCCGAGGACTGACGGCTTTCGGGGCCGCTCTGTAGACGC 3051  
 Qy 3061 CATCGCGCATCACCGACCCGAGAGGACATCCAGGACTTTGTCTCTACGCGGCACTG 3120  
 Db 3052 CATCGCGCATCACCGACCCGAGAGGACATCCAGGACTTTGTCTCTACGCGGCACTG 3111  
 Qy 3121 AGCAGACACCGCGCGGTACACCAACAAGCGCTGCGCCACCTGACGGTGTATTACAAG 3180  
 Db 3112 AGCAGACACCGCGCGGTACACCAACAAGCGCTGCGCCACCTGACGGTGTATTACAAG 3171  
 Qy 3181 CTCATGCGCCCGCGCGGCTCCCTCCATCAAGGACCGGATCCCGTACGTGATCGTG 3240  
 Db 3172 CTCATGCGCCCGCGCGGCTCCCTCCATCAAGGACCGGATCCCGTACGTGATCGTG 3231  
 Qy 3241 GCCAGACCGCGAGGTAGAGGAGCGGTGCGCGGTGCGCGCTCCCGGAGCTAGAC 3300  
 Db 3232 GCCAGACCGCGAGGTAGAGGAGCGGTGCGCGGTGCGCGCTCCCGGAGCTAGAC 3291  
 Qy 3301 GCGCGCCCGCGAGGACGAGCCCGCCCGGCGGCTGCGCTCCCGGAGCGC 3360  
 Db 3292 GCGCGCCCGCGAGGAGCGCGCCCGCGGCTGCGCTCCCGGAGCGC 3351  
 Qy 3361 CCCCGGAGACGCGTGCATGCGACCCCGCGGAGCGGTCCAAAGCCCGGCAAGCTG 3420  
 Db 3352 CCCCGGAGACGCGTGCCTGCGACCCCGGAGCGGTCCAAAGCCCGGCAAGCTG 3411  
 Qy 3421 CTGGTGTCCGAGCTGGCGGAGATCCCGGCTAGCCATCCCGGGCGTTCGCTCAAC 3480  
 Db 3412 CTGGTGTCCGAGCTGGCGGAGATCCCGGCTAGCCATCCCGGGCGTTCGCTCAAC 3471  
 Qy 3481 ACGGACTATTACTTCTCGCACTCTGCGGGCGGCTGCGTGCATGCTTCAAGGCGCTGTTT 3540  
 Db 3472 ACGGACTATTACTTCTCGCACTCTGCGGGCGGCTGCGTGCATGCTTCAAGGCGCTGTTT 3531  
 Qy 3541 GGAATAACGCAAGATCACCGAGGTCTGTAAAGAGGTTTATTCGCGAGAGCTGGCAC 3600  
 Db 3532 GGAATAACGCAAGATCACCGAGGTCTGTAAAGAGGTTTATTCGCGAGAGCTGGCAC 3591  
 Qy 3601 CCCCGGAGACGCGTGGCGCGGCTCAGGGCGCGGCTTCCGGCGCGGGCGCGG 3660  
 Db 3592 CCCCGGAGACGCGTGGCGCGGCTCAGGGCGCGGCTTCCGGCGCGGGTGGGTCGCGC 3651  
 Qy 3661 GCTACGCGGAGGAACTCTGCGAATGTTGATAGAGCTTGTATCTCTAGCATGA 3717  
 Db 3652 GCTACGCGGAGGAACTCTGCGAATGTTGATAGAGCTTGTATCTCTAGCATGA 3708

RESULT 9  
 ID ADP74211/c  
 XX ADP74211 standard; DNA; 149158 BP.  
 AC ADP74211;  
 XX  
 DT 26-AUG-2004 (first entry)  
 XX  
 DE Equine herpesvirus 1 genome gM deletion mutant #2.  
 XX  
 KW virucide; vaccine; Equine Herpes Virus; EHV; gM; vaccine;  
 KW EHV-associated condition; Equine herpesvirus 1; EHV1; db; mutant; mutein.  
 OS  
 OS Equine herpesvirus 1.  
 OS Synthetic.  
 XX  
 PN US2004109873-A1.  
 XX  
 PD 10-JUN-2004.  
 XX  
 XX 21-JUL-2003; 2003US-00624149.  
 PF  
 XX 19-JUL-2002; 2002DE-01033064.  
 PR  
 PR 14-AUG-2002; 2002US-0403282P.  
 PR  
 PR 11-APR-2003; 2003DE-01017008.  
 XX

PA (BOEH ) BOEHRINGER INGELHEIM VETMEDICA GMBH.  
 XX Neubauer A, Ziegler C;  
 XX WPI; 2004-440311/41.  
 XX  
 PT New recombinant equine herpes (EHV) virus free of heterologous elements,  
 PT and where protein gM has been deleted, useful as a vaccine for treating  
 PT or preventing EHV infections.  
 XX  
 PS Claim 9; Page; 156pp; English.  
 XX  
 CC The invention describes a new recombinant Equine Herpes Virus (EHV) where  
 CC the protein gM is absent, and the EHV is free of heterologous elements.  
 CC Also described are: a nucleic acid coding for an EHV defined above; a  
 CC vaccine preparation comprising the EHV or nucleic acid; obtaining a  
 CC recombinant EHV; and a cell line for use in the method, where the gene  
 CC encoding the protein gM is transfected into the cell line, and the cell  
 CC line expresses gM. The vaccine comprising the EHV or nucleic acid  
 CC encoding EHV is useful for treating and/or preventing EHV-associated  
 CC condition, and for monitoring the therapeutic success. The recombinant  
 CC EHV is useful as a vaccine against EHV infections. This sequence  
 CC represents an equine herpesvirus 1 genome in which nucleotides 93268-  
 CC 94322, comprising regions of the gM gene, have been deleted.  
 XX  
 SQ Sequence 149158 BP; 32350 A; 42892 C; 41659 G; 32257 T; 0 U; 0 Other;  
 Query Match 29.7%; Score 1104.8; DB 12; Length 149158;  
 Best Local Similarity 59.1%; Pred. No. 1.6e-169;  
 Matches 2131; Conservative 0; Mismatches 1317; Indels 156; Gaps 8;  
 Qy 186 GGCCTAGCGCATACGTACTACAGCGAGTGCAGCAATTTTCGATTTATCGCCCGCTTC 245  
 Db 55065 GCCCCCCCAACATCTGTAACGACAGGTGGGTAGCTTTAAGTTTATAGCTCCAAGATG 55006  
 Qy 246 GCTGGAAGAGACGCGCCCGCGAGCAGCGACCGGGGTCCACGACGCGCGCTCCGCGG 305  
 Db 55005 CCTCGATGAAGAAGCCCCCGCGACGACGCGGTGTACAGCTGGCGCACCTTGGAGCG 54946  
 Qy 306 CGCCCTTAGGTCTACTGCGGGGGGACGAGCGGAGTCTCCGCGTGGCGCGCGAGGG 365  
 Db 54945 CCCACCCAAAGTGTACTGCGATGGCTCAGAGTACGAGCTGTAACCTTTCCTCCGAGG 54886  
 Qy 366 CTCTGCGCGCGTCTGCGCTTGGCGCTGCGGGCGGTGGCGACCATCGCCCGCAAGGGGTTCTGA 425  
 Db 54885 TTGCTGGCTCGAGGATTCGGGTGTGAAGCGCCAGGATTTTCGGGGCGATGGATTCAA 54826  
 Qy 426 CCCACCGCTCACCGTCTTCCACGTGTACGACATCTCTGGAGCAGCTGGAAACACGCGTACAG 485  
 Db 54825 CCCAGATTTGAGAGATTTTCACTGTACGACATAGTAGAGACTTCGGAGAGCGCTCACA 54766  
 Qy 486 CATGCGCGCGCGCGCTCCACGAGGATTTATGGAGCCCATCACGCGCCCGCGGACCGT 545  
 Db 54765 CGATGACCCATCCAGGTTTCTGAGCTAT-----CCGCGCAAGCGGCTCTGT 54718  
 Qy 546 CATCAGCGCTTCTGGGTCTGACCCCGCAAGGCCCATCGCGTCCGCTTTCACGCTTACGCGCAC 605  
 Db 54717 GGTAAACACTCTGGGAATGAGCGAGTGTGAAGCGAGTTCGCGTTCACGCTATGCTGT 54658  
 Qy 606 GCGCGAGTACTTTTATACATGAACAAAGCGGAGGTGGATCG----- 644  
 Db 54657 GCGCCATTTATTTTACATGGCAAAGCGGAGGTGGATAGCGCTTGTGGAATAACACCGGA 54598  
 Qy 645 -----GCACCTGCAGTGGCGTCCCGCGCG-----GATCTCT 676  
 Db 54597 GGCAGAACTCTGCGCGCAATGTTGAGTCTCGCGCAAGCTCGGCTTTGAGCGCGGCTCT 54538  
 Qy 677 GCGAGCGCTTGGCGCGCGCGCTCGCGAGTTCGCGGGGGCGGTCTGTTCCGCGG----- 728  
 Db 54537 GGGAAATGGCAACGCGCGGCAACACAGAGCGCGGAGTGGTGGGCGGAAA 54478  
 Qy 729 ---CATCTCCGCGGACCACTTCAGAGCGGAGGTGGTGGAGCGCGCGCGCTGTACTATTATTA 785

Db 54477 GCACGTGTCGGGACTGCTTCAAGTGGAGACCGGTGTCACACGACGCTGTACTACTT 54418  
Qy 786 CGAAACGCGCCGACCCCTGTACTACCGCGTCTTGTCGGAAGCGGCGCGCTGGCCTA 845  
Db 54417 TGGATCTAAGCCAGCTCTCTACTATAGATATCTGCCTCCAGACGCGCTGGAGGGTT 54358  
Qy 846 CTTGTGCGACAACTTTTCCCGCGGATCAGGAAGTACGAGGGGGGCTGACGCGCAAC 905  
Db 54357 CATCTGCGACAACTTTTCAACCGGAGATTACAAAATTCGAGGGGAGCGTGGACGTCAC 54298  
Qy 906 CCGGTTTATCTGGAACACCCGGGGTTGTCACTTCCGCTGGCTGTACCGCTCAAGCCCGG 965  
Db 54297 CGGCTGTGTGACATGAATTTTACAGTTTCGGGTGGTACCGCTGGACCCCG 54238  
Qy 966 CCGGGGAAACGCGCGGCCCAACCGCGCCCGACGCGCTTCGGAACCTCGACGACGT 1025  
Db 54237 CACCCACGAGAGCGTGTCAACTTCGCCCGCTTGAGCGACACGTCACCTCAAGCGAGT 54178  
Qy 1026 CGAGTTTAACTGACGGCGGACAACTTGGCCGCTCGAGGGGGCCATGTGTGACCTGGCGGC 1085  
Db 54177 GGAGATTAACTGTACTCCCGATAACCTGGAGCCGATACGACGAGGCTGCCTGGCCCGA 54118  
Qy 1086 CTACAAGCTCATGTCTCGATATCGAATGCAAGCGCGGGGGGAGGACGAGCTGGCCTT 1145  
Db 54117 CTATAAGCTCATGTCTTGTATATAGAGTGTAAAGCTGGAACGGGTAAACGAAATGGCGTT 54058  
Qy 1146 TCCGGTCCGGAAACCGCGGAAGACCTGCTCATCCAGATCTCTGTCTGTACTACGACCT 1205  
Db 54057 CCCAGTGGCAACTAACCAAGAGACCTGTGTCATCCAGATCTCTGTCTGTGTAATCGCT 53998  
Qy 1206 GTCACACACCGCTCGAGACATCTCTCTCTGTTTTTTCGTTGCTGCGACCTCCCGGA 1265  
Db 53997 TGCTACTCAGAACACGCAACACACCTCTGCTTTTCCCTCGGCTCATGCGATATCTCTGA 53938  
Qy 1266 GTCCCACTCAGCATCTGCGCTCCAGGGCTCCGCGCCCGCTGCTGCTGCGATTGA 1325  
Db 53937 GGAATACTCGTTTGCATGCTCCAGCGCGCGAGCCGAGCCGAGCGGTTTGGAGTTGA 53878  
Qy 1326 CAGCGAATTCGAGATGCTGTGGCTTCATGACCTTCGTCAAGCAGTACGCGCCCGAGTT 1385  
Db 53877 CAGCGAGTACGAGCTGTGTTGCTTCTGACCTTCTCAAGCAGTACTCTCCCGAGTT 53818  
Qy 1386 CTTGACCGGGTACAACTATCATCTTGCAGTGGCCCTTGTCTGACCAAGCTGACGGA 1445  
Db 53817 CGCCACCGGCTACAACTCGTTAATTTTGACTGGCGGTACATAGTTAAACAGGTAAAGTC 53758  
Qy 1446 GATCTACAAGTCCCGCTCGACGGGTACGGCGCATGAACGCGCGGGTGTGTTCCCGT 1505  
Db 53757 GGTGTATAACATCAAGCTGACGGGTACGGCAAGTTCAACAAAGGGGGGCTGTTTAAAGT 53698  
Qy 1506 GTGGACATCGGCCAGACCACTTTCAGAGCGCAGCAAGATCAAGGTGAACGGGATGGT 1565  
Db 53697 GTGGACATCGCCACGAACCACTTTCAGAGAGGCAAGGTGAATCAATGSCCTGAT 53638  
Qy 1566 GAACATCGACATGTACGGCATCATACCGCAAGGTCAAACTCTCCAGCTACAAGCTGAA 1625  
Db 53637 ATCTCTAGACATGTATTCTGGCGGACGGAAGCTAAAGCTACCCAGCTACAACTCGA 53578  
Qy 1626 CGCGTCCCGAGCGCTCTTGAAGGACAGAGAGAGATGAGCTACCGGACATCCC 1685  
Db 53577 CGGGTCTGGGAGACGCTCTCGCGAGCATTAAGATAGACCTTCCCTATAAAGAAATACC 53518  
Qy 1686 CGCCTACTAGCCTCCGGGCCGCGAGCGGGGTGATCGGCGAGTATTGTGTCAGGA 1745  
Db 53517 CTCCTATTACGGGAGGGCTGACCGAGGGGGTAAATAGGAGATTGTATCCAGGA 53458  
Qy 1746 CTGCTCTGTGCGGAGCTGTTTCTTCAAGTTTCTCCGCACTCGGAGCTTTCGCGCT 1805  
Db 53457 CTCTAGGCTGTGGGCAAGCTGTTTTTAAAGTACCTCCCCATCTGGAACCTATCGGCGGT 53398  
Qy 1806 CGCGCGCTGGCGGCATCAACATCACCGCACCATCTACGACGGCCAGCAGATCCGCT 1865  
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Qy 1866 CTTTCACTGCTCCTGCGCCTTGGCGCCAGAAAGGCTTTCATCTGCGGACACCCAGGG 1925  
Db 53337 GTACACGTGCTGTGAAATCTGCGCCGGAGAGAAATTTTCAATTTGCGAGACACAGACG 53278  
Qy 1926 GCGGTTTCGGGCTCTCGACAAAGAGGCGCCCAAGCGCCGCGCTGCTCGGG----- 1978  
Db 53277 CCGGTTTGAAGTTCAGGACAGCGCGGCTCAGAGACTTCGAGATTGGCTATGGAAGCA 53218  
Qy 1979 -----GGGAAGGGAGCGCGCGGGACGGAAACGGGGACAGGATAGAGACGACGCA 2033  
Db 53217 AAGCCACGCTTCGACAGTACAGACGAAACCGGACGCTGTGACGCTACCCGAGACGCGC 53158  
Qy 2034 GGACGAGAGCGGACGAGCGGAGGAGTTCGCGCGGAGACCGGGGGCGCGACGTTGG 2093  
Db 53157 AGGATCTGGCGCTACTTCTGAAACGGAGCGGGAAGCCCGGCTGCGGAGGGCGTGG 53098  
Qy 2094 GTACAGGGGGCCCGGCTCTCGACCCCAACCTCCGGGTTTCACTGACACCCGTTGGT 2153  
Db 53097 CTACAGGGAGCAAGGTTCTTAGACCCGCTATCCGGCTTTTCACTGGAACCCCGTGGT 53038  
Qy 2154 GTTTGACTTTGCGAGCTGTACCCAGCATCATCCAGCCACACCTGCTGCTTCAGTAC 2213  
Db 53037 GTTTGACTTCTGAGCTTTATACCCAGCAATATCCAGGCCATTAACCTCTGTTTACCAC 52978  
Qy 2214 GCTCTCCTCGCGGCCGAGCGCTGCGGCACCTGAGGCGGACCGGACTACTCTGGAGAT 2273  
Db 52977 CTTGGCGCTCGATGAAGTGGATCTGGCGGGCTTCAACCATCCGCTGACTACTCGAGT 52918  
Qy 2274 CGAGGTGGGGGCGGACGCGTGTTCGTGGAAGGCCCAAGTACGCGAGAGCCTGCTGAG 2333  
Db 52917 CGAGGTGGGTGACCAAAAGTTATTTTGTGTCACGCCATATTCGCAAGGCTGCTGG 52858  
Qy 2334 CATCTGCTCGCGAGCTGGCTGGCCATGCGAAAGCGGTGAGGCGCGGAATCCCCACAG 2393  
Db 52857 CATCTGCTCGCGAGCTGGCTGGCCATGCGAAAGCGGTGAGGCGCGGAATCCCCACAG 52798  
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Db 52797 CACCCCGAGAGGCGAGTCTTACTAGATAGAGCAGTCTGCGATTAAAGGTGATGCA 52738  
Qy 2454 CTGCGTGTACGCGTTTACCGGGGCGGACGCTGCTTCTGCGCTTGCCTGCTGACAGTGGCGC 2513  
Db 52737 CTGCGTTTACGAGTATCAACGGGGTGGCAACCGGCTGTGCGGTCTGAGGAGTAGCGC 52678  
Qy 2514 CACGTTGACCACTCGCGCGCGAGATGCTCTCGCGACGCGCGCTACGTTGACAGCGC 2573  
Db 52677 TACCGTTACCAAGATAGGACGCGACATGCTCTCAAGACCGGAGATTACGTTCACTCTC 52618  
Qy 2574 CTGGCGGAGTTCGATCAGCTGCTGGCGGACTTTTCCGAGGCGCGCGCATGCGCGCCC 2633  
Db 52617 TTGGCGGACGCGGAGCTGCTGGAGGACAAATTTTCCAGGGGCTATAGTTTCCGAACCA 52558  
Qy 2634 CGGTGCGTACTCCTATGCGCATCATCTACGGGACACGACTCCATTTTGTGTTGTCGG 2693  
Db 52557 CAAGCCTTACTCGCTCAGGGTATCTACGGAGACACGACTCCGCTGTTTATCAAGTTGT 52498  
Qy 2694 CGGCTCAGCGCGCGGCTGTTGGCCATGGGGGCAAAAGTGGGAGCCACATCTCGC 2753  
Db 52497 GGGCTGACGTAAGAGGGGTATCGGAGCTGGGGGATGCTATGTCGCGTCAGATTTCAGC 52438  
Qy 2754 CGGCTGTTCTCTCCCGGATCAAGCTCGAGTGGAAAAACGTTTCAACAGCTGCTGCT 2813  
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Qy 2814 CATCGCAAGAAAAAGTACATCGCGCTCATCTCGGGGGCAAGATGCTCATCAAGGGCGT 2873  
Db 52377 GATCACCAAGAAAGTACATAGTGTGCAATAACGGGGGGAAGATGCTCATTAAGGGGGT 52318  
Qy 2874 GGATCTGGTGGCAAAACAACTGCGGTTTATCAACCGCACCTTCCAGGGCGCTGCTGCA 2933  
Db 52317 CGACCTGGTCCGCAAAATAACTGCTCTTTCATAAACTTGTACGCGCGACATCTGGTAGA 52258







QY	645	-----GACCTGCGAGTCCGTCGCCCGCGC-----GATCTCT	676	Db	53517	CTCCTATTACCGGAGGGCTGACCGGAGGGCGTAATAGAGAGTATTGTATCCAGGA	53458
Db	54597	GGCAGAACTGCTGCGCAATGGTGGACTGCGGCACAGCTCGGCTTTGAGCGGGCCT	54538	QY	1746	CTCGTGTGCTGGGAGCTGTTCTTCAAGTTCGCGGCACCTGGAGCTTTCGCCGT	1805
QY	677	GGGAGGCTGGCGGGCCCTGCGGAGTCCCGGGGGCGTCTGCCGG-----728		Db	53457	CTTAGGCTGTGGGCAAGCTGTTTTTAAAGTACCTCCCATCTGGAACTATCGCGGT	53398
Db	54537	GGGAAATGGCAACGGCGGCAACAGAGCGGGCGACGCGCGGGGATGGTGGGCGGAAA	54478	QY	1806	CGCGCGCTGGCGGCATCAACATCACCCGACCATCTACGACGGCGAGCAGATCCGGT	1865
QY	729	---CATCTCCGCGGACCACTTCGAGCGGAGGTGGAGCGCGCGCGAGTGTACTATTA	785	Db	53397	GGCCAAACTCGCCGTATCACCTAAACGGGGGTAAATTTTGAOGGTGAGCAATTCGGT	53338
Db	54477	GCACGTGCTCGGAGCTGTTCAAGTGGAGACCGTGTGCCACAGACGCTGTACTATT	54418	QY	1866	CTTCAOGTGTCTCTGCGCTTGGGGCCAGAAAGGCTTTCATCTCTGCGGACACCAAGG	1925
QY	786	CGAAACGCGCCGACCTCTGTAATAACCGCTCTTCGTGCGAAGCGGGCGCGCTGGCCTA	845	Db	53337	GTACACGTGCTGTCTGAACTCGCGCGGAGAGAAATTTCAATTTTCCAGACAACAGACG	53278
Db	54417	TGGATCTAAGCGAGCTCTCTACTATAGAGTATCTGCTCCAGCAGCGCTGGAGGGT	54358	QY	1926	GGGTTTTGGGGCTTCGACAGAGGAGCGCCCAAGCGCGCGCGCTCGCTCGG-----1978	
QY	846	CCTGTGCGACAACTTTTCCCGCGATCAGGAGTACAGAGGGGGCTGCGGCCACAC	905	Db	53277	CCGGTTGACAGTCAGGAGACGCGCGTTCAGAGACTTTCCGAGTTGGCTATGGATAGCCA	53218
Db	54357	CATCTGCGACAACTTTTCAACCGGAGATTACAAATTCAGAGGGAGCGTGGACAC	54298	QY	1979	-----GGGAGGGGAGCGCGCGGGGACGGGAAACGGGACGAGGATAAGGACGACGA	2033
QY	906	CCGGTTTATCTTGGAACAACCGGGGTTTTGTCACTTTCGGCTGTGTACCGCTCAAGCCCGG	965	Db	53217	AAGCCACGCTTCGACAGTACAGACGAAACCGACGGTGTGACGGTATCCCGGACGCGC	53158
Db	54297	GGGCTGTTGTTGGACATGAATTTTACAGTTTTCCGTTGGTGTACCGCTCGGACCGG	54238	QY	2034	GGAAGGAGACGGGACGAGCGGAGAGGTGCGCGCGAGACCGGGGGCGGCACTGTGG	2093
QY	966	CGCGGGAAACGCGCGGCCCAACCGCGCCCCCGGACGCGGTTTGGAACTTCGAGCGAGT	1025	Db	53157	AGGATCTGGCGCTACTTCTGAAACCGGAGCGGGAAGCCCGCGTCTGGGAGGGCGGTGG	53098
Db	54237	CACCCACGAGAGCGTGTCAACTTCGCGCGGTTTGAGCGACACGTCACCTCAAGCGAGCT	54178	QY	2094	GTACAGGGGGCGGGTCTCGACCCACTCTCGGGTTTCACTCGACCGCGTGGTGT	2153
QY	1026	CGAGTTTAACTGCGGCGGACCACTTGGCGCTCGAGGGGGCCATGTGTGACCTGCCGC	1085	Db	53097	CTACAGGAGCAAAAGTTCTAGACCCCGTATCCGCTTTTATGTGGACCCCGTGGTGT	53038
Db	54177	GGAGTTAACTGTATCTCCGATATACCTGGAGCGGATACGACGAGGCTGTCTGCCCGA	54118	QY	2154	GTTTGACTTTTCCAGCCTGTACCCAGCATCATCCAGGCCCAACCTGTGCTTCAGTAC	2213
QY	1086	CTAAGCTCATGTGCTTCGATATCGAATGCAAGGCCGGGGGAGGAGCTGGGCTT	1145	Db	53037	GTTTGACTTCTGCTAGCTTTATACCAAGCATTTATCCAGGCCCATTAACCTCTGTTTACCCAC	52978
Db	54117	CTAAGCTCATGTGCTTCGATATAGAGTGTAAAGCTGGAAGGGTAAAGAAATGGCGT	54058	QY	2214	GCTCTCCTGCGGCGGAGCGCTGCGGCACTCGGAGGCGGACCGGGACTACTTGAGAT	2273
QY	1146	TCCGGTCCGGAAACCCCGGAAGACTCGTCATCGAGTCTCTGTCTGTCTACGACCT	1205	Db	52977	CCTGGCGCTCGATGAAGTGGATCTGGCGCGGCTTCAACCATCCGTCGACTACTCGACGTT	52918
Db	54057	CCAGTGGCAACTAACCAAGAGGACCTGTCATCCAGATCTCTCTGTCTGTACTGCT	53998	QY	2274	CGAGTGGGGGCGGCGGCTGTTCTGTAAGGCCCACTACGCGAGAGCTGCTGAG	2333
QY	1206	GTCCACACCGCTCGAGGACATCTCTGTTTTCGCTCGGATCTCGGACCTCCCGA	1265	Db	52917	CGAGTGGGTGACCAAAAGTTATTTTGTCCAGCCCATATTCGCGAAAGCTGCTTGG	52858
Db	53997	TGCTACTCAGAACCAAGCAACACCTGCTGTTTTTCCCTCGGGTCATGCGATATCTCTGA	53938	QY	2334	CATCTCTGCGGACCTGGCTGGCATGCGAAAGCAGATCCGCTCGCGGATCCCCAGAG	2393
QY	1266	GTCCACCTCAGCGATCTCGCTCCAGGGGCTGCGCGGCCCGCTGCTCTGGAAGTTGA	1325	Db	52857	CATCTGCTGCGGACCTGGCTGGCCATGCGGAAAGCGGTGAGGGCGCAATCCCAACAG	52798
Db	53937	GGATATCTGTTGATCGCTCCAGCGGCGGAGCCGAGCGGTTTTGAGATTGA	53878	QY	2394	CACCCCGAGGAGCGGCTCTCTCGCAAGCAACAGCGGCCCATCAAGGTGGTGTGCAA	2453
QY	1326	CAGGAAATCGAGATGCTGTGGCTTCATGACCTTCGTCAAGCAGTACGCGCCCGAGTT	1385	Db	52797	CACCCCGAGGAGGACGTTTACTAGATTAAGCAGCAGTCTCGATTAAGGTGATATGCAA	52738
Db	53877	CAGCGAGTACGAGCTGTGTTGCTTCTGACCTTTCTCAAGCAGTACTCTCCCGAGTT	53818	QY	2454	CTCGGTACGGGTTTCCCGGGCGGAGCAGCGTCTTCTGCGCTGCTGCAAGTGGCGC	2513
QY	1386	CGTACCGGGTACACATCATCACTTCGATGCGCCCTTCTCTGACCAAGCTGACGGA	1445	Db	52737	CTCGGTACGGAATTCACGGGGTGGCAACGGCTGTTTGGCTGCTGAGGATAGCGCG	52678
Db	53817	CGCACCGGCTACAACTCATGTTTGAATTTGACTGGGCGTACATGTTTAAAGGTAAAGTC	53758	QY	2514	CACCGTACCAACCATCCGCGCGGAGATGCTCTCGCGACGCGCGCTGCTGCGCGCG	2573
QY	1446	GATCTCAAGGTCCCGCTCGACGGGTACGGCGGATGAAACGGCGGGGTGTTTCCGGT	1505	Db	52677	TACCGTTACCAAGTACGACGCGATGCTCTCAAGACCGAGATTAAGTTCACTCTCG	52618
Db	53757	GGTGTATACATCAAGCTGGAGGGTACGGCAAGTTCAACAAAGGGGGCTGTTTAAAGT	53698	QY	2574	CTGGGCGGAGTTTCATCAGCTGTGGCGCATTTTTCGGAGGGCGCGGCGGCGCC	2633
QY	1506	GTGGACATCGGCGAGACCACTTTCAAGCGGAGCAAGATCAAGGTGAACGGGATGGT	1565	Db	52617	TTGGGCGACGCGCGAGCTGTGGAGGACAAATTTTCCAGGGGCTATAGGTTTCCGAAACCA	52558
Db	53697	GTGGGACATCGCCACGAACCAATTTTCAAGAGAGCAAGGTGAATAATGCGCTGAT	53638	QY	2634	CGGTCTGCTTCCATGCGCATCTATACGGGACACGAGCTCCATTTTCTGTTTGTGCGG	2693
QY	1566	GAAATCGACATGTACGCATCATCACCGACAAGGTCAAATCTTCCAGCTCAAGCTGAA	1625	Db	52557	CAAGCTTACTCTCGTCAAGGTTATCTATCGGAGACACCGACTCCGCTGTTTATCAAGTTGT	52498
Db	53637	ATCTCTAGACATGTTTCTGTGGCGACGGAAGCTAAAGCTAACCCAGCTACAAACTCGA	53578	QY	2694	CGGCTCAACGCGCGCGCTTGGTGGCCATGCGGCGCAAAAGTGGCGAGCCACATCTCGG	2753
QY	1626	CGCGTCCGCGAGGCGCTTGTGAAGGACAAGAAAGGATCTGAGCTACCGCGACATCCC	1685	Db	52497	GGGCTCAGCTACAGAGGGGTATCGGAGCTGGGGATGCTATGTGCGGTGAGATTTACG	52438
Db	53577	CGCGTGTGGGAGAGCTCTCGGCGGAGCATAGATAGACCTTCCCTATAAAGAAATACC	53518	QY	2754	CGGCTGTTTCTTCCCGCGGATCAAGCTCGAGTGCAGGAAACGTTTCAACAGCTGCTGCT	2813
QY	1686	CGCCTACTACGCTCCCGGCGCGGAGCGCGGGGTGATCGGCGAGTATTGTGTGAGGA	1745				

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Db 52437 GGACCTCTTTAGAGCGCCATCAAACTGGAGTGTGAGAGACCTTTTCAGCGACTGTGCT 52378
Qy 2814 CATGCCCAAGAAAAGTACATCGCGTCACTCGGGGGCAAGATGCTCATCAAGGCGT 2873
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Qy 2874 GGATCTGGTGGCAAAACAACTCGCGTTTATCAACCCGACCTCCAGGCGCTGTGCGA 2933
Db 52317 CGACCTGGTGGCAAAATAACTTGTCTTTTCATAACTTGTAGCGCGCATCTGTAGA 52258
Qy 2934 CCTGCTGTTTTTACGAGATACCGTATCCGGAGCGCGCCGCTTACCGAGCGCCCGC 2993
Db 52257 TCTTTTGTGTACGACGAGGATGTGGCCACGCGCGCAGCAGAGTGCACAGCGTCTCC 52198
Qy 2994 AGAGGAGTGTGCGCGGACCCCTGCGCGAGGAGTGCAGCGCTTCGGGCGCTCTCGT 3053
Db 52197 CGCAGAAATGGGTGGGGCGCCGCTTACCGAGCGCTTTTGACAGCTTTGGGCGAGTGTGGT 52138
Qy 3054 AGACGCCATCGCGCGCATACCGACCGGAGAGGACATCCAGACTTTTGTCTCACCGC 3113
Db 52137 AGAGCGTACAAACGTTACTGTGCCCACTTTGGAGCTGCGGAGTTCGTTATGACTGC 52078
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Db 52077 TGAGCTGAGCGGCTCACCCGAATCGTATACCAACAAAGCGCTGCGGCACCTCACCGTCA 52018
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Db 52017 CTTTAAAGCTGCCATGAGGAATGAAGAACTGCCGAGCGTAAAGAGAGAATTCGTTATGT 51958
Qy 3234 GATCGTGGCCAGACCCGCGAGGTAGAGGAGCGGTGCGCGGCTGGCGCCCTCCGCGA 3293
Db 51957 GATAGTTGCGAGACC-----GAGGCCGCGGACCGGA 51925
Qy 3294 GCTAGAGCGCGCGCCCGCAGGGAGAGCGCGCCGCCAGCGGCCCTGCCCTCCCGCGC 3353
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Qy 3354 CAAGCGCCCGGGAGAGCGCGTCCGATCGGACCCCGCGGAGCGCTCCAGGCCCG 3413
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Qy 3414 CAAGCTCTGCTGTGTCGAGTGGCGGAGGATCCGGGTAGCCCATCGCCGGGCGGTTC 3473
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Qy 3534 CCTGTTTGGAAATAACCCCAAGATCACCGAGAGTCTGTTAAGAGGTTTATTCGCGAGAC 3593
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Qy 3594 GTGGCAC- - -CCCCCGGACGACGTGGCGCGCGGCTCAGGGCGCGGGGTTCCGGCGCGC 3650
Db 51666 CCCCCAAGACCCCAAGAAACCCAGGCACCTGCTTGGAGCGCGCGCTTTGAAAGCT 51607
Qy 3651 GGGGGCGCGCGCTACCGCGGAGGAACTCGTCGATGTTGATAGACCTTTGATCTCT 3710
Db 51606 GACGCCCTTTACACCGGAGGAAGTCTGTCGAATACTGCATACAGTTTTTTTGTACTCT 51547
Qy 3711 AGCA 3714
Db 51546 AGAA 51543
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RESULT 11

ADP74216/c

ID ADP74216 standard; DNA; 150071 BP.

XX

AC ADP74216;

XX

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DT 26-AUG-2004 (first entry)
XX Equine herpesvirus 1 genome gM deletion mutant #1.
DE virucide; vaccine; Equine Herpes Virus; EHV; gM; vaccine;
XX EHV-associated condition; Equine herpesvirus 1; EHV1; ds; mutant; mutein.
KW Equine herpesvirus 1.
OS Synthetic.
XX US2004109873-A1.
XX 10-JUN-2004.
XX 21-JUL-2003; 2003US-00624149.
XX 19-JUL-2002; 2002DE-01033064.
XX 14-AUG-2002; 2002US-0403282P.
XX 11-APR-2003; 2003DE-01017008.
XX (BOEH ) BOEHRINGER INGELHEIM VETMEDICA GMBH.
XX Neubauer A, Ziegler C;
XX WPI; 2004-440311/41.
XX New recombinant equine herpes (EHV) virus free of heterologous elements,
PT and where protein gM has been deleted, useful as a vaccine for treating
PT or preventing EHV infections.
XX Claim 8; Page; 156pp; English.
XX The invention describes a new recombinant Equine Herpes Virus (EHV) where
CC the protein gM is absent, and the EHV is free of heterologous elements.
CC Also described are: a nucleic acid coding for an EHV defined above; a
CC vaccine preparation comprising the EHV or nucleic acid; obtaining a
CC recombinant EHV; and a cell line for use in the method, where the gene
CC encoding the protein gM is transfected into the cell line, and the cell
CC line expresses gM. The vaccine comprising the EHV or nucleic acid
CC encoding EHV is useful for treating and/or preventing EHV-associated
CC condition, and for monitoring the therapeutic success. The recombinant
CC EHV is useful as a vaccine against EHV infections. This sequence
CC represents an Equine herpesvirus 1 genome in which nucleotides 93268-
CC 93318 and 94222-94322, comprising regions of the gM gene, have been
CC deleted.
XX Sequence 150071 BP; 32583 A; 43129 C; 41914 G; 32445 T; 0 U; 0 Other;
SQ Query Match 29.7%; Score 1104.8; DB 12; Length 150071;
Best Local Similarity 59.1%; Pred. No. 1.6e-169;
Matches 2131; Conservative 0; Mismatches 1317; Indels 156; Gaps 8;
Qy 186 GGTCTAGCGCCATACGTACTACAGCGAGTGCAGAGTGGGTAGTCTTTAAGTTTATAGCTCCAAGATG 245
Db 55065 GCCCCCCCAACACTCGTACTGCACAGAGTGGGTAGTCTTTAAGTTTATAGCTCCAAGATG 55006
Qy 246 GCTGGACGAGACGCGCCCCCGGAGCAGCGCACCGGGTCCACGACCGCGCCCTCCGCGC 305
Db 55005 CCTCGATGAGAGAGCCCCCGCCGACCGACGACGCGGTGTACACGTGGGACCTTGGAGCG 54946
Qy 306 CGGCCCTAAGGTGTACTGCGGGGGGAGCAGCGGAGCTCTCGCGGTGGGCCCGCGAGGG 365
Db 54945 CCCACCCAAAGTGTACTGCGATGGCTCAGAGTACGACGTCTGAACCTTTGCGCTCCGAGG 54886
Qy 366 CTTCTGCGCGCTCGCTTGGCGCTGTGGGCGGTGGGACCATGCCCCCAAGGGGTTCGA 425
Db 54885 TTGCTGGCTCCGAGGATTCGGGTTTGGAAACGCCAGGATTTTCGGGGCGATGATTCAA 54826
Qy 426 CCCACCGCTCACCGTCTTCCACGTGTACGACATCTCGAGACAGTGTGAACACGCGGTACAG 485
Db 54825 CCCAGATTTGAGAGATTTTCACGTGTACGACATAGTAGAGACTTCGGGAGAGCGCTCACA 54766
Qy 486 CATGCGCGCGCCGACGTCTCCACGAGGATTTATGGAGCCCATCAGCCCCCGCGGACCGT 545
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Db	54765	CGATGACCATCCAGGTTTGTGAGCTAT-----CCCGCCCAAGCGGCTCTGT	54718	Db	53697	GTGGGACATCCCGACGAACCACTTTTTCAGAGAAGAGCAAGGTGAATAAATCAATGGCCTGAT	53638
Qy	546	CATCAGCTTCTGGGTTCTGACCCCGAAGGCCATCGCGTGGCGGTTTCAGCTCTACGGCAC	605	Qy	1566	GNAATCCACATGTACGGCATCATCACGACAAGGTCAAACTCTCCAGCTACAGCTGAA	1625
Db	54717	GGTAACATGCTGGGAATGAGCGAGTGTGGAAAGCGAGTCGCGGTTTACAGTCTATGGTGT	54658	Db	53637	ATCTCTAGACATGATTTCTGTGGCGACGGAAGCTAAAGCTACCCAGCTACAACTCGA	53578
Qy	606	GGCGAGTACTTTTATCATGAACAAGCGGAGGTGGATCG-----	644	Qy	1626	CGCGTCCCGGAGGCGGCTTTTGAAGGACAGAAGAAGGATCTGAGCTTACCGCGACATCCC	1685
Db	54657	GGCCCATTTATTTTATATGCAAAAGCGGAGGTGGATAGCGCTTGTGGAAATAACACCGA	54598	Db	53577	CGCGTCTGTGGAGACGCTCTCGGCGACATAAGATAGACCTTCCCTATAAGAATAACC	53518
Qy	645	-----GCACCTGAGTCCGTCGCCCGC-----GATCTCT	676	Qy	1686	CGCCTATACCGCTCCGGGCCCGCGACGCGGGGTGATGCGCGAGTATGTGTGAGGA	1745
Db	54597	GGCAGAACTCGTGGCGCAATGGTGAATGCGCGCACAGCTCGGCTTTGAGCGCGGCCCT	54538	Db	53517	CTCCTATTACCGGAGGCGCTGACCGGAGGCGGTAAATAGGAGAGTATGTATCCAGGA	53458
Qy	677	GGAGCGCTGGCGCGGCCCTGCGCGAGTCCCGGGGCGTTCGCGG-----	728	Qy	1746	CTCGTCTGCTGGGAGCTGTTCTTCAAGTTTTCGCGCACCTGGAGCTTTCGCCGT	1805
Db	54537	GGGAATGGCAACGGCGCAACAGACAGCGCGGCGAGCGCGGGGATGGTGGGCGGAAA	54478	Db	53457	CTTAGGCTGTGGGCAAGCTGTTTTTAAAGTACCTCCCCCATCTGGAACCTATCGCGGT	53398
Qy	729	---CATCTCGCGGACCACTTCGAGCGGAGGTGGTGGAGCGCGCGACGCTGTACTATTA	785	Qy	1806	CGCGCGCTGGCGGGCATCAACATCACCGCACCATCTACGACGGCCAGCAGATCCGGT	1865
Db	54477	GCACGTGTCTGGGACTGCTTCAAAGTGGAGACCGTGTGCCACACGAGCTGTACTT	54418	Db	53397	GGCCAAACTCGCCGCTATCACCTAAACGCGGGTAAATTTTGAOGTCAAGCAATTCGGT	53338
Qy	786	CGAAACGGCCCGACCTGTACTACCGGTCTTCGTGCGAAGCGGCGCGCTGGCCCTA	845	Qy	1866	CTTCACTGTCCTCTCGCGCTTGGGGCCAGAAAGGCTTTCATCTGCGGACACCAAGG	1925
Db	54417	TGGATCTAAGCCAGCTCTACTATAGAGTATCTGCCTCCAGCAGCGCCTGGAGGGT	54358	Db	53337	GTACACGTGCTGTGTAACCTCGCCCGCGAGAGAAAATTTCAATTTTGCAGACAAACAGACG	53278
Qy	846	CCTGTGCGACAACTTTTGCCTCGCATCAGGAAGTACGAGGGGCGTCCAGCCACCAC	905	Qy	1926	GCGGTTTCGGGGCTCGACAGGAGGCGCCCAAGCGCCGCGCTCTCGG-----	1978
Db	54357	CATCTGCGAACAATTTACCGGAGATTACAAAATTCAGGGGAGCGTGGACGTACAC	54298	Db	53277	CCGTTTGAACAGTCAGGACGCGCGCTCAGAGCTTTCGAGTGGCTATGGATAGCCA	53218
Qy	906	CGGTTTATCTCGGAACAACCGGGGTTTGTCACTTTCGGCTGTGTACCGCCTCAAGCCCGG	965	Qy	1979	-----GGGAAGGGAGGCGCGCGGGACGGGAACGGGACAGGATTAAGACGACGAGA	2033
Db	54297	CGGCTGTTTGGACAATGAAATTTTACCAGTTTCGGTGGTGTACCGCTCGGACCGG	54238	Db	53217	AAGCCACGCTTCGACAGTACAGACGAAACCGACGGTGTGACGGTACCCCGGACCGCG	53158
Qy	966	CGCGGGAAACGGCGCGCCCAACCGCGCCCGGACGGGTTTGGAACTCGAGCGAGCT	1025	Qy	2034	GGAAGAGAAACGGGACGAGCGGAGGAGTTCGCGGCGAGACCGGGGCGCGGACGTTGG	2093
Db	54237	CACCCACGAGAGCGTGTCAACTTCGCGCCCGTTGAGCGACACGTCACCTCAAGCGAGT	54178	Db	53157	AGGATCTGGCGCTACTTCTGAAAACGGAGGCGGAAGCCCGCGTTCGGAGGGCGGTGGG	53098
Qy	1026	CGAGTTTAACTGACGGCGGACAACTCGCGCTCGAGGGGCCATGTGTGACCTCGCGG	1085	Qy	2094	GTACAGGGGGCGCGGCTCTCGACCCACCTCGGGGTTTCACTCGACCCGCTGGTGT	2153
Db	54177	GGAGTTAACTGTATCTCCGATACCTGGAGCGGATACAGAGGCTGCTGCGCCCGA	54118	Db	53097	CTACAGGAGCAAAAGTTCTAGACCCCGCTATCCGGCTTTCATGTGGACCCCGTGGTGT	53038
Qy	1086	CTACAAGCTCATGTCTTCGATATCGAATGCAAGGCCGGGGGAGAGACGAGCTGGCTT	1145	Qy	2154	GTTTGACTTTTGCCACGCTGTACCCAGCATCATCCAGGCCCAACCTGTCTCAGTAC	2213
Db	54117	CTATAAGCTCATGTCTTGTATATAGTGTAAAGCTGGAACGGGTAAAGAAATGGCTT	54058	Db	53037	GTTTGACTTCGCTAGCTTATACCCAAAGCTTATCCAGGCCATTAACCTCTCTTCCACAC	52978
Qy	1146	TCGGTTCGCGGAAACGCGCGGAGACCTCGTCAATCCAGATCTCTGTCTGTCTACGACT	1205	Qy	2214	GCTCTCCTCGCGCCGAGCGCGTTCGCGACCTGGAGGCGGACCGGAGTACCTGGAGAT	2273
Db	54057	CCCAAGTGGCAACTAAACCAAGAGGACCTGTCATCCAGATCTCTGTCTGTCTGCT	53998	Db	52977	CCTGGCGCTCGATGAAGTGGATCTGGCGGGCTTCAACCATCCGTCGACTACTCGACGT	52918
Qy	1206	GTCCACCAACCGCTCGAGACATCTCTCTGTTTTCGCTCGGATCCCTGCGACCTCCCGA	1265	Qy	2274	CGAGTGGGGGGCGACGGCTGTTCTTGTGMAAGGCCCAAGTACGCGAGAGCTGCTGAG	2333
Db	53997	TGCTACTGAAACACAGAACACACCTGCTGTTTTCCTCGGGTCAAGCATATCTCTGA	53938	Db	52917	CGAGTGGGTGACCAAAAGTTATTTTGTCCAGCCCATATTCGCGAAAGGCTGCTGG	52858
Qy	1266	GTCCCACTCGAGCATCTCGCTCCAGGGGCTGCGCGGCCCGCTGCTGCGAGTTTGA	1325	Qy	2334	CATCTCTCTCGGACCTGGCTGGCCATGCGAAGACAGATCCGCTCGGGATCCCGCAGAG	2393
Db	53937	GGAATACTCGTTTGCATCGTCCAGCGCGGCGAGCCAGACGAGGTTTGGAGTTGA	53878	Db	52857	CATCTCTCTCGGACCTGGCTGGCCATGCGAAGGCGGTGAGGGCGGATCCCGACAG	52798
Qy	1326	CAGGAATTCAGATGCTGTGGCTTCATGACCTTCGTCAAGCAGTACGCGCCCGAGTT	1385	Qy	2394	CACCCCGAGAGGCGCGCTCTCTCGAACAAGCAAACGCGGCCCATCAAGGTGGTGA	2453
Db	53877	CAGGAGTACGAGTGTGTGTGCTTCCCTGCTGTTTTCCTCGGGTCAAGCATATCTCTGA	53818	Db	52797	CACCCCGAGAGGCGAGTCTTACTAGATAGCAGCAGTCTGCGATTAAGGTGATGAA	52738
Qy	1386	CGTCAACGGGTACAACTCAATCTGACCTGCGCTTCGCTCGTCCAGCAGCTGACGGA	1445	Qy	2454	CTGGTGTACGGGTTCAACGGGGGCGAGCGGTCTTCTGCCCTGCTGACGTTGGCGG	2513
Db	53817	GGCACCAGGCTACAACTGCTTAATTTTGAATGGGCGTACATAGTTTAAAGGTAACGTC	53758	Db	52737	CTGGTTTACGGATTCACGGGGGTGGCAACCGGCTGTTCCGCTCTGAGGATAGCGGC	52678
Qy	1446	GATCTACAAGTCCCGCTCGACGGGTACGGCGCATGAACGGCGGGGTGTTTCCGCT	1505	Qy	2514	CACCGTGACCAACCATCGGCGCGAGATGCTCTCGGACGCGCGCTGACGTCACCGCG	2573
Db	53757	GGTGTATAACATCAAGCTGACGGGTACGGCAAGTTCAACAAAGGGGGCTGTTTAAGT	53698	Db	52677	TACCGTTACCAAGTAGGACGCGACATGCTCTCAAGACCGGAGATTAAGTCTACTCTG	52618
Qy	1506	GTGGACATCCGCGAGAGCCACTTTTCAGAAACGCGACGAAGATCAAGGTGAACCGGATG	1565	Qy	2574	CTGGCGGAGTTCGATCAGCTGTGGCCGACTTTTCGGAGGCGGCGGATGCGCGCCC	2633
				Db	52617	TTGGCGAGCGCGAGCTGCTGGAGGACAATTTTCCAGGGGCTATAGGTTTTCGAAACCA	52558

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Qy 2634 CGGTCCGTACTCATGCGCATCATCTACGGGGACACGAGTCCATTTTCGTTTGTGCGG 2693
Db 52557 CAAGCCCTTACTCCGTGAGGGTTATCTACGGAGACACCGACTCCGTGTTTATCAAGTTGT 52498
Qy 2694 CGGCTCACGGCCGGCGCTGTGGGCATATGGGCGACAAAGATGGCGAGCCACATCTCGCG 2753
Db 52497 GGGCTGACGTACGAGGGGGTATCGGAGCTGGGGATGCTATGTCTCGGTGATTTTCAGC 52438
Qy 2754 CGGCTGTTCTCTCCCGCATCAAGCTCGAGTGGAAAAAGTTTACCAAGCTGTGCT 2813
Db 52437 GGACCTCTTTAGAGCGCCATCAAACTGGAGTGTGAGAAGACCTTTTCAGCGACTGCTGCT 52378
Qy 2814 CATGCCAAGAAAAGTACATCGCGCTCATCTGCGGGGCAAGATGCTCATCAAGGCGT 2873
Db 52377 GATCACCAGAAGAAGTACATAGGTGTATAAACCGGGGGGAAGATGCTCATGAAGGGGT 52318
Qy 2874 GGATCTGGTGGCAAAAAAACAATGCGGCTTTATCAACCGCACCTTCCAGGGCCCTGTGCGA 2933
Db 52317 CGACCTGGTCGCAAAAATAACTGCTCTTTTCATATAACTTTGTACGCGGACATCTGTAGA 52258
Qy 2934 CTGCTGTTTACGACATACCGPATCCGGAGGCGCGCGCTTACCGAGCGCCCCCG 2993
Db 52257 TCCTTTGTTGTACGACGAGGATGTGGCCACGGCGCAGCAGAGTGACAGACGTGCTCC 52198
Qy 2994 AGAGGAGTGTGGCGGACCCCTGCGGAGGAGTCTCAGGCGTTTCGGGCGCTCTCGT 3053
Db 52197 CGCAGAAATGGTGGGGCGCCGCTTACCGAGCGGCTTTTGACAAAGTTTGGGCGAGTGTGCT 52138
Qy 3054 AGACGCCATCGGGCGATCACCGACCGGAGAGGAGCATCCAGGACTTTGTCTCACCGC 3113
Db 52137 AGAGCGTACACCGTATCTACTGCCCCCACTGGACGTGGCGAGTTCTGTATGACTGC 52078
Qy 3114 CGAATCGAGCAGACACCGCGCGGTATACCAACAGCGCTGCGCCCACTGACGGTGA 3173
Db 52077 TGAGCTGAGCGCTCACCGCAATCTATACCAACAGCGCTGCGCCACCTCACCGCTA 52018
Qy 3174 TTACAAGCTATGGCGCGCGCGAGTCCCGTCCATCAAGAGCCGATCCGCTACGT 3233
Db 52017 CTTTAAGCTGCCATGAGGAATGAAGAACTGCCAGCGTAAAGAGAGAATTCGTTATGT 51958
Qy 3234 GATCGTGGCCAGACCGCGAGGTAGAGAGACGGTGGCGGCTGGCCGCTCCCGCA 3293
Db 51957 GATAGTTGGCAGACC-----GAGGCGCGGAACGGA 51925
Qy 3294 GCTAGACGCGCGCGCGCGAGAGAGCGCGCGCGCGCGCGCTGCTCCCGCG 3353
Db 51924 AGCGGGTGTAGTAAACTCAATGCGCGGTACCGCGCCAAAACCCCGTGTAAACCAAGACCGC 51865
Qy 3354 CAAGCGCGCGCGGAGACGCGTGCATGCGACCCCGCGGAGGCGCTCCAGCCCG 3413
Db 51864 ACGCCCCAACCTAA-----ACG 51847
Qy 3414 CAAGCTGTGTGTCCGAGCTGGCGGAGATCCCGGGTACGCCATCCCGGGCGGTTC 3473
Db 51846 CARACTGTGTGTTCGAGCTCGCGAAGACCGACCTATGTTTCCGGAATGACGTACC 51787
Qy 3474 GCTCAACACGACATTTACTTCTCGACCTGCTGGGCGCGCTGCGTACGTTCAAGC 3533
Db 51786 GCTAAACACAGACTACTATTTCTCCCACTGTGGGTACCAATAAGCGTACCTTTAAGC 51727
Qy 3534 CCGTGTGGAAATAACGCCAAGATCACCGAGAGTCTGTTAAAGAGGTTTATTCGAGAC 3593
Db 51726 TCTATTCGAAATGATGTGAGAAACAAGAAAATCTTTAAAGCGGTTTATTCGGAAC 51667
Qy 3594 GTGGCAC---CCCCCGAGCAGCTGGCGCGCGCTCAGGGCCCGGGGTTTCGGGCGCGC 3650
Db 51666 CCCCCACAAGACCCCAAGAAAACCCAGGCACCTGTTGAGCGCGCGGCTTTGAAAAGCT 51607
Qy 3651 GGGGGCGCGCTACGGCGGAGGAACTCGTCAATGTTGATAGAGCTTTGATCTCT 3710
Db 51606 GACGCCCTTTTACCGGAGGAGAAAGTGTGCAATACTGCAATACAGTTTTTTTGTACTCT 51547

Qy 3711 AGCA 3714
Db 51546 AGAA 51543

RESULT 12
ADP74201/c
ID ADP74201 standard; DNA; 150223 BP.
XX
AC ADP74201;
XX
DT 26-AUG-2004 (first entry)
XX
DE Equine herpesvirus 1 genome seqid 1.
XX
KW virucide; vaccine; Equine Herpes Virus; EHV; gm; vaccine;
KW EHV-associated condition; Equine herpesvirus 1; EHV1; ds.
XX
OS Equine herpesvirus 1.
XX
PN US2004109873-A1.
XX
PD 10-JUN-2004.
XX
PF 21-JUL-2003; 2003US-00624149.
XX
PR 19-JUL-2002; 2002US-01033064.
PR 14-AUG-2002; 2002US-0403282P.
PR 11-APR-2003; 2003DE-01017008.
XX
(BOEH ) BOEHRINGER INGELHEIM VETMEDICA GMBH.
XX
Neubauer A, Ziegler C;
XX
WPI; 2004-440311/41.
XX
New recombinant equine herpes (EHV) virus free of heterologous elements,
PT and where protein gm has been deleted, useful as a vaccine for treating
PT or preventing EHV infections.
XX
Disclosure; SEQ ID NO 1; 156pp; English.
XX
The invention describes a new recombinant Equine Herpes Virus (EHV) where
CC the protein gm is absent, and the EHV is free of heterologous elements.
CC Also described are: a nucleic acid coding for an EHV defined above; a
CC vaccine preparation comprising the EHV or nucleic acid; obtaining a
CC recombinant EHV; and a cell line for use in the method, where the gene
CC encoding the protein gm is transfected into the cell line, and the cell
CC line expresses gm. The vaccine comprising the EHV or nucleic acid
CC encoding EHV is useful for treating and/or preventing EHV-associated
CC condition, and for monitoring the therapeutic success. The recombinant
CC EHV is useful as a vaccine against EHV infections. This sequence
CC represents the Equine herpesvirus 1 genome.
XX
SQ Sequence 150223 BP; 32615 A; 43173 C; 41953 G; 32482 T; 0 U; 0 Other;
Query Match 29.7%; Score 1104.8; DB 12; Length 150223;
Best Local Similarity 59.1%; Pred. No. 1.6e-169;
Matches 2131; Conservative 0; Mismatches 1317; Indels 156; Gaps 8;
Qy 186 GGTCTAGCGCCATACGTTACTACGCGAGTGGCGAGAAATTCGATTTATCGCCCGCGTTC 245
Db 55065 GCCCCCCAACACTCGTACTGCACAGAGTGGGTAGCTTTAAAGTTTATAGCTCCAAGATG 55006
Qy 246 GCTGGACAGAGACGCCCGCGGAGCAGCACCGGGGTCCAGCGCCGCTCCCGCG 305
Db 55005 CCTCGATGAAGAAGCCCCCGGACCGAGCGGGTACACGTGGGACCTTTGGAGCG 54946
Qy 306 CGCCCTTAAGGTGTACTGCGGGGGGACGAGCGCGAGTCTCTCCGCGTGGGCCCGGAGGG 365
Db 54945 CCCACCCAAAGTGTACTGCGATGCTCAGAGTACAGAGTGTGAACCTTTGCTCCGAGG 54886
Qy 366 CTTCTGGCGCGTCTGCTTGTGCGCTGTGGGGGCGGTGGGACCATGCCCCCAAGGGGTTTCA 425
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Db	54885	TTGCTGGGCTCCAGGATTCGGGTTTGAAGCGCCAGGATTTTCGGGGCGATGGATTCAA	54826	Db	53817	CGCACCGGCTCAACATCGTTAAATTTTACTGGCGGTACATATGTTAAACAAGGTAAACGTC	53758
Qy	426	CCCCACCGTCAACGCTTCTCCAGTGTACGACATCTGAGCAGCGTGGAAACACGCGTACAG	485	Qy	1446	GATCTACAAGTCCCGCTCGACGCGGTACGGCGCATGAACGCGCGGGTGTGTTCCGCGT	1505
Db	54825	CCCCAGATTGAGAGATTTCAGTGTACGACATAGTAGAGACTTCGGAGAGCGCTACA	54766	Db	53757	GGTGTATAATCAATCAAGCTGGACGGGTACGGCAAGTTCAACAAGGGGGGCTGTTTAAGT	53698
Qy	486	CATGCGCGCGCCAGCTCCACGAGCGATTTATGGACGCCATACGCCCGCGGACCGT	545	Qy	1506	GTGGACATCGGCGCAGAGCCACTTTTCAGAACGCGCAGCAAGATCAAGGTGAACGGGATCGT	1565
Db	54765	CGATGACCCATCCAGGTTTGTGAGCTAT-----CCGCCCCAAGCGGTCTGT	54718	Db	53697	GTGGGACATCGCCACGAACCATTTTTCAGAAAGAGCAAGGTGAATAATCAATGGCCTGAT	53638
Qy	546	CATCAGGCTTCTGGGTCTGACCCCGAAGGCCATCGCTCGCGCTTACGTTCTACGGCAC	605	Qy	1566	GAAATCGACATGTACGGCATCATCCGACAAAGTCAAACTCTCCAGCTACAGCTGAA	1625
Db	54717	GGTAACACTGTGGGAATGAGCGAGTGTGGAAAGCGAGTCGCGGTTCACGCTATGCTGT	54658	Db	53637	ATCTCTAGACATGTTATTTCTGTGGCGCGGAAAGCTAAAGCTACCCAGCTCAAACTCGA	53578
Qy	606	GCGGAGTACTTTTACATGAACAAGCGGAGGTGGATCG-----	644	Qy	1626	CGCGCTCGCCGAGCGCTTCTTGAAGGACAAGAAGAGTCTGAGCTACCGGACATCCC	1685
Db	54657	GCGCATTATTTTACATGGCNAAGCGGAGGTGGATAGCGTTGTGGAAATAACACCGGA	54598	Db	53577	CGCGTGTGGGAGACGCTCTCGGGGAGCATTAAGATAGACCTTCCCTATAAAGAAATACC	53518
Qy	645	-----GCACCTGCAGTGCCTGCCCGCGC-----GATCTCT	676	Qy	1686	CGCCTACTACGCTCCGCGGCCGCGAGCGGGGTGATCGGCGAGTATTGTGTGACGGA	1745
Db	54597	GGCAGAACTCGTGGCGCAATGGTGGACTGCGCGCACAGCTCGGCTTTGAGCGGCGCT	54538	Db	53517	CTCCTATTACGCGGAGGGCTGACCGGAGGGCGTAAATAGAGAGTATTGTATCCAGGA	53458
Qy	677	GCGAGCGCTGGCGCGCCCTGCGGAGTCCCGGGGGCGTGTTCGCGG-----	728	Qy	1746	CTCGCTGCTGCTCGGGGAGCTGTTCTTCAAGTTTCTGCGGACCTTGAGGCTTTCGCGCT	1805
Db	54537	GGGAAATGGCAACCGCGCAACAGAGCGGGCGAGCGCGGGGGATGGTGGGGCGGAAA	54478	Db	53457	CTCTAGGCTGTGGGCAAGCTGTTTTTAAAGTACTCCCCATCTGGAACCTATCGCGCGT	53398
Qy	729	---CATCTCCGCGGACCACTTCGAGGCGGAGGTGGGAGCGCGGAGTGTACTATTA	785	Qy	1806	CGCGCGCTGCGGGGCATCAACATCACCCGACCATCTACGACGCGCAGCAGATCCGCGT	1865
Db	54477	GCAGTGTCTCGGACTGCTTCAAGTGGAGACCGGTGTCACACGAGCTGTACTCT	54418	Db	53397	GGCCAAACTCGCCGCTATCACCTAACGCGGTTAAATTTTGACGCTCAGCAATTCGCT	53338
Qy	786	CGAAACGCGCCGACCCCTGTACTACCGGCTCTTGTGGAAGCGGCGCGCTGGCCTA	845	Qy	1866	CTTCACGCTGCTCTCGCGCTTTCGGGCGCAGAAAGGGCTTCATCTCGCGGACACCCAGG	1925
Db	54417	TGGATCTAAGCCAGCTCTCTACTATAGATATCTGCCTCCAGACCGCTTGGAGGGTT	54358	Db	53337	GTACAAGTCTGTGTAACCTCGCCCGGAGAGAAATTCATTTCGACAGACACAGACG	53278
Qy	846	CCTGTGCAACAATTTTCCCGCGGATCAGGAAGTACGAGGGGGCGTFCAGCGCACAC	905	Qy	1926	CGCGTTTCGGGGCTTCGACAAAGGAGCGCCCAAGCGCCGCGCTGCTCGGG-----	1978
Db	54357	CATCTGCGACAACTTTACCGCGGAGATTACAAAATTCAGGGGAGCGTGGACGTGACCA	54298	Db	53277	CCGTTTGTACAGTCAGGACGACGCGCGTTCAGAGACTTCGAGTTGGCTATGATAGCA	53218
Qy	906	CCGTTTATCTGGACAAACCGGGTTGTACCTTGGCTGTGCTGCTACCGCTCAAGCCGG	965	Qy	1979	-----GGGAAGGGAGCGCGCGGGGACGGGAACGGGAGCAGAGATTAAGACGACGAGA	2033
Db	54297	CGCGCTGTGTGGACAATGAATTTTACCAGTTTGGGTGGTACCGCTTCGACCCCGG	54238	Db	53217	AAGCCAGCTTCGACAGTACAGACGAACCGGACGCTGAGCGGTACCCGCGACCGCGC	53158
Qy	966	CCGCGGAAACCGCGCGCCCAACCGCGCCCGACGCGCTTCGGAACCTCGAGCGACGT	1025	Qy	2034	GGACGAGACGGGACGAGCGCGAGGAGTTCGCGCGGAGACCCGGGGCGCGGCGCTTGG	2093
Db	54237	CACCCAGGAGCGGTGTTCACTTCGCCCGTTCGAGCGACGTCACCTCAAGGACGT	54178	Db	53157	AGGATCTGCGCTACTTCTGAARAACGAGCGGGAAGCCCGCGCTCGGAGGGCGTGG	53098
Qy	1026	CGAGTTTAACTGCAACGCGGCAACCTGGCGCTCGAGGGGCCATGTGTGACCTGCCGCG	1085	Qy	2094	GTACAGGGGGCGCGGTCTCGACCCCACTTCGCGGTTCACGTCGACCCCGTGTGGT	2153
Db	54177	GGAGATTAACTGTACTCCCGATAACCTGGAGCCGATACCAGACGAGGCTGCTGGCCCGA	54118	Db	53097	CTACAGGGAGCAAAAGTTCTAGACCCCGTATCGCGCTTTCATGTGGACCCCGTGTGT	53038
Qy	1086	CTACAAGCTCATGTGCTCGATATCGAATGCAAGCCGGGGGAGGACGAGCTGGCCTT	1145	Qy	2154	GTTTGACTTTGCGAGCTGTACCCAGCATATCCAGGCGCCACAACTGTGCTTCAGTAC	2213
Db	54117	CTATAAGCTCATGTGCTTGTATATAGATGTAAAGCTGGAAACGGGTAAACGAATGGCGTT	54058	Db	53037	GTTTGACTTCGCTAGCTTATACCAAGCATATTCAGGCGCCATAAATCTGTGTTTACCAC	52978
Qy	1146	TCCGCTCGCGAAACGCGCGGAAGACCTCGTATCCAGATCTCTGTCTGCTCTACGACCT	1205	Qy	2214	GCTCTCCCTCGCGCCCGAGCGCTGCGCGACCTGAGGCGGACCGGACCTACCTGGAGAT	2273
Db	54057	CCAGTGGCAACTAACCAAGAGGACCTGTGTCATCCAGATCTTCTGCTGCTGCTGCTGCT	53998	Db	52977	CTGGCGCTCGATGAAGTGGATCTGGCGGGCTTCAACCATCCGTCGACTACTCGAGCT	52918
Qy	1206	GTCCACCAACCGCTTCGAGCAATCTCTCTGTTTTTTCGCTGGGATCTTCGCACTCCCGA	1265	Qy	2274	CGAGGTGGGGGCGGACGCGTGTTCCTGTAAGGCCCAAGTACGCGAGAGCCTGCTGAG	2333
Db	53997	TGCTACTCAGAACCAAGCAACACCTGCTGTTTTTCCCTCGGGTCATGGGATATCTCTGA	53938	Db	52917	CGAGTGGGTGACCAAAAGTTATTTTGTGTCACGCGCCATATTCGCGAAGCCCTGCTGG	52858
Qy	1266	GTCCCACTCAGGATCTGCGCTCGAGGGGCTGCGCGCCCGCTGCTGCTGGAGTTGA	1325	Qy	2334	CATCTGCTCGGCGACTGGCTGGCCATGCGAAGCAGATCGCTCGCGGATCCGCCAGAG	2393
Db	53937	GGAACTACTCTGTTGATGCTGTCAGCGCGGCGAGCCAGACCGAGCGTTTGGAGTTGA	53878	Db	52857	CATCTGCTCGGCGACTGGCTGGCCATGCGAAGGCGGTGAGGCGCGGAATCCCCCAACG	52798
Qy	1326	CAGCGAATTCAGATGCTGTGGCTTCATGACCTTGTCAAGCAGTACGCGCCCGAGTT	1385	Qy	2394	CACCCCGAGAGCGCGCTCTCTCTCGACAAGCAACAGCGCGCCATCAAGGTGGTGTGCA	2453
Db	53877	CAGGAGTACAGCTGCTGTGTTGCTTCTGACCTTCTCAAGCAGTACTCTCCCGAGTT	53818	Db	52797	CACCCCGAGAGGCGAGTTTACTAGATAAGCAGCAGTCTGCGGTTAAGGTGATATGCA	52738
Qy	1386	CGTACCGGGTACACATCATCAACTTGCAGTGGCGCTTCTGCTGACCAAGCTGACGGA	1445	Qy	2454	CTCGGTGTACGGGTTCACCGGGCGCAGCAGGCTTCTGCTGCTGCTGCTGCAAGTGGCGC	2513
				Db	52737	CTCGTTTACGGATTTCACGGGGGTGGCAACGGCGCTGTTGCGGTGCTGAGGATAGCGCG	52678

QY	2514	CACGTCACGACCATCGGCGCGAGATGCTCCTCGCGACGCGCGGTACGTGACGCGCG	2573	QY	3594	GTGGCAC--CCCGCGGACGACGTGCGCGCGGTCTGAGGCGCGCGGGTTGCGGCGCGC	3650
Db	52677	TACGTTACACGATAGGACGCGACATGCTCTCCACAGACCGAGATTACGTTCACTCTCG	52618	Db	51666	CCCCCAAGACCCCGCCAGAAACCCAGGCACTGCTTGAGCGCGCGGCTTTGAAAAGCT	51607
QY	2574	CTGGCGGAGTTTGGATCAGCTGCTGCGCGATCTTTCCGAGAGCGCGCGGATGCGCGCCCC	2633	QY	3651	GGGGGCGCGGCTACCGCGGAGGAACTCGTGAATGTTGCATAGAGCCCTTGTACTCT	3710
Db	52617	TTGGGCGACGCGGAGCTGCTGGAGGACAATTTTCCAGGGGCTATAGTTTTCGAAACCA	52558	Db	51606	GAGCCCTTTACACCGGAGGAAAGTCGTCGAATCTGCACTACACATGTTTGTACTCT	51547
QY	2634	CGGTCCGTACTCCATGCGATCATCTACGGGGAACGGAATCCATTTTCTGTTGTCGCG	2693	QY	3711	AGCA 3714	
Db	52557	CAAGCCTTACTTCGCTAGGGTTATCTACGGAGACACCGACTCCGCTGTTTATCAAGTTGT	52498	Db	51546	AGAA 51543	
QY	2694	CGGCTCACGCGCGCGCTGCTGGCCATGCGGCGACAAAGATGCGGAGCCACATCTCGCG	2753	RESULT 13			
Db	52497	GGGCTGACGTACGAGGGGTATCGGAGCTGGGGATGCTATGTCGGCTCAGATTTCAGC	52438	ID	ADJ95524		
QY	2754	CGGCTGTTCTCCCGCGATCAAGCTCGAGTGGAGTGAAGAAACGTTTACCAAGCTGCTCT	2813	XX	ADJ95524	standard; DNA; 3663 BP.	
Db	52437	GGACCTCTTTAGAGCGCCATCAAACTGGAGTGTGAGAGACCTTTTTCAGCGACTGCTGT	52378	XX	ADJ95524;		
QY	2814	CATCGCCAGAAAGTACATCGCGTCACTCGGGGGCAAGATGCTCATCAAGGCGCT	2873	XX	06-MAY-2004	(first entry)	
Db	52377	GATCACCAGAAGATGATAGTGTCTATAACCGGGGGAAGATGCTCATGAAGGGGT	52318	XX	Equine herpesvirus type 1	ORF30 gene sequence.	
QY	2874	GGATCTGCTGCGCAAAACAACTGCGGCTTTATCAACCGCACCTTCCAGGCGCTTGTGCGA	2933	XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
Db	52317	CGACCTGTCGCGCAAAATAACTGCTTTTCAATAAATTTGACGGCGACATCTGGTAGA	52258	XX	Equine herpesvirus type 4; genetic marker; ORF30-ml region marker;		
QY	2934	CTGCTGTTTACGATACGATACGATACCGAGGCGCGCGCTTACCGAGCGCCCCCGC	2993	XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
Db	52257	TCCTTTGTTGTACGACGAGGATGCGCACCGCGCGGAGAGTGACAGACGTCGCTCC	52198	XX	Equine herpesvirus type 4; genetic marker; ORF30-ml region marker;		
QY	2994	AGAGGAGTGTGCGCGACCCCTGCGCGAGGAGTCTGACGCGTTCGGGCGCGTCTCT	3053	XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
Db	52197	CGCAGATGGTGGGCGCGCGCTTACCGAGCGGCTTTGACAAGTTTGGGCGAGTCTGGT	52138	XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
QY	3054	AGACGCCATCGGCGCATCACCGACCGGAGAGGAGATCCAGGACTTTTCTCTCACCGC	3113	XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
Db	52137	AGAGCGGTACAAACGATATCATCTGCCCACTTGGAGCTGCGCGAGTTCGTTAGCTGC	52078	XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
QY	3114	CGAATGAGAGACACCGCGCGGTACACCAACGAGCGCTGCGCCACCTGAGCGTGA	3173	XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
Db	52077	TGAGCTGAGCGCTCACCGAACTGATATCAACCAAGCGCTGCGCACCTCACCGTCTA	52018	XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
QY	3174	TTCAAGCTCATGCGCGCGCGAGTCCCGTCCATCAAGGACCGGATCCGTACGT	3233	XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
Db	52017	CTTTAAGCTCGCATGAGGAATGAGAACTGCGCAGCGTAAAGAGAGAAATTCGTTATGT	51958	XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
QY	3234	GATCGTGGCCAGACCGCGAGGTAGAGAGACGCTGCGCGGCTGGCGCCCTTCCCGCA	3293	XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
Db	51957	GATAGTTGCGCAGAC-----GAGCGCGGGAACGCA 51925		XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
QY	3294	GCTAGACGCGCGCGCGGAGAGCGCGTCCGATGCGACGCGCGCGCGCGCGCGCGCGC	3353	XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
Db	51924	AGCGGCTGTAGTAACTCAATGCGCGGTACCGCGCCCAAAACCCGTTGTAACCAAGACCGC	51865	XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
QY	3354	CAAGCGCGCGCGGAGAGCGCGTCCGATGCGACGCGCGCGCGCGCGCGCGCGCGCGC	3413	XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
Db	51864	ACGCCCCAACCTAA-----ACG 51847		XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
QY	3414	CAAGCTGCTGCTGTCGAGTGGGAGGATCCGGGTAGCCCATCCCGGGCGGTTC	3473	XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
Db	51846	CAAACTGCTGTTTCCGACCTCGCGAAGACCGACCTATGTTTCCGAGAATGACGTACC	51787	XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
QY	3474	GCTCAACAAGATATTACTTCTGCACTGCTGGGGCGCGCTGCTGAGCTTCAGGC	3533	XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
Db	51786	GCTAAACACAGACTACTATTCTCCCACTGTTGGGTACCATAGCGCTGTTTAAAGC	51727	XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
QY	3534	CCTGTTTGGAAATAACCGCAAGATCAACGAGAGTCTGTAAAGAGGTTTATTCGCGAGAC	3593	XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		
Db	51726	TCTATTCCGAAATGATGTGAGAACACAGAAATCTTTAAAGCGGTTTATTCGGAAC	51667	XX	virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4;		

Query Match 29.6%; Score 1100; DB 12; Length 3663;  
Best Local Similarity 59.0%; Pred. No. 9.4e-169;  
Matches 2128; Conservative 0; Mismatches 1320; Indels 156; Gaps 8;





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Db 2268 CGAGTGGGTGACCAAAAGTTATTTTGTGTCACGCCATATTCGCGAAAGCCTGCTGG 2327
Qy 2334 CATCTGCTCGGGACTGGCTGGCCATGCGAAAGCAGATCCGTCGCGGATCCCCAGAG 2393
Db 2328 CATCTGCTCGGGACTGGCTGGCCATGCGAAAGCGGTGAGGCGCGAAATCCCCACCAG 2387
Qy 2394 CACCCCGAGGAGCGCTCTCTCGACAAGCAACAGCGGCCCATCAAGGTGGTGTGCAA 2453
Db 2388 CACCCCGAGGAGCGAGTTTACTAGATAAGCAGCAGTCTGCGATTAAAGTGATGCAA 2447
Qy 2454 CTGCGTGTACGGGTTCACCGGGCGCAGCAGCGTCTTCGCGCTGCTGCTGACGTCGCGC 2513
Db 2448 CTGCGTTTACGGATTACCGGGGTGGCAACCGGCTGTTCGCGGTCTGAGGATAGCGC 2507
Qy 2514 CACGTGACGACCATCGCGCGGAGATGCTCTCGCGACGCGCGCTACGTGACGCGCG 2573
Db 2508 TACCGTTTACACGATAGGACGCGACATGCTCTCAAGACCGAGATTACGTTCACTCTCG 2567
Qy 2574 CTGGGCGAGTTTCGATCAGCTGCTGGCGGACTTTCCGGAGCGCGCGCATGCGCGCCCC 2633
Db 2568 TTGGGCGACGCGGAGCTGTGCGGACAAATTTCCAGGGGCTATAGTTTCCGAACCA 2627
Qy 2634 CGGTCCGTACTCCATGCGCATCATCTACGGGACACGGAATCCATTTTCGTTGTGCGG 2693
Db 2628 CAAGCCTTACTCCGTACGGGTATATCTACGGAGACACCGACTCCGTGTTTATCAAGTTGT 2687
Qy 2694 CGGCTCACGGCGCGGCTGTGGCCATGCGGACAGATGGCGACACATCTCGG 2753
Db 2688 GGGCTCACGTACGAGGGGTATCGGAGCTGGGGATGCTATGTGCGGTGAGATTTTCAGC 2747
Qy 2754 CGGCTGTTCTCCGCCCGTCAAGCTCGAGTCGAGTGCAGAAACGTTACCAAGCTGCTGCT 2813
Db 2748 GGACCTCTTAGAGCGCCATCAAACTGGAGTGTGAGAACCTTTTCAGCGACTGCTGCT 2807
Qy 2814 CATCGCAAGAAAGTACATCGCGCTCATCTCGGGGCAAGATGCTCATCAAGGCGT 2873
Db 2808 GATCACCAAGAAGTACATAGTGTCTATAAACCGGGGGAAGATGCTCATGAAGGGGT 2867
Qy 2874 GGATCTGTCGGCAAAACACTCGCGGTTTATCAACCGCACCTCCAGGGCCCTGTGCGA 2933
Db 2868 CGACCTGTCGCAAAAATAACTGCTCTTCAATAACTTGTACGCGGACATCTGGTAGA 2927
Qy 2934 CCTGCTGTTTACGACGATACGCTATCCGGAGCGCGCGCTTAGCGGAGCGCCCGC 2993
Db 2928 TCTTTTGTGTACGACGAGATGTGGCCACGCGGCGAGCAAGGTGACAGCTGCTCC 2987
Qy 2994 AGAGGAGTGTGCGCGACCCCTGCGCGAGGAGTGCAGCGGTTGCGGCGCGTCTCGT 3053
Db 2988 CGCAGATGGGTGGGGCGCGCTACCGAGCGGCTTTGACAAGTTTGGCGGAGTGTGTT 3047
Qy 3054 AGAGCCCATGCGGCGATCACCGACCGGAGAGGACATCCAGGACTTTGCTCTACCGC 3113
Db 3048 AGAGGCGTACAACCGGTATCATGCGCCCACTTGGACGTGCGCGAGTTCGTTAGTGC 3107
Qy 3114 CGAACTGAGCAGACACCGCGCGGTACACCAACAGCGCTGCGCCACCTGACGGTGA 3173
Db 3108 TGAGCTGAGCGGCTCACCGGATCGTATACCAACAGCGCTGCGGACCTCACCGTCTA 3167
Qy 3174 TTCAAGCTCATGGCCCGCGCGCGAGGTCCCGTCCATCAAGGACCGGATCCCGTACGT 3233
Db 3168 CTTTAAAGCTCGCCATGAGGAATGAAGAACTGCCCGAGCTGAAAGAGAGAAATTCGTTATGT 3227
Qy 3234 GATCGTGGCCAGACCCGCGAGGTAGAGGAGACGCTGCGCGGCTGCGGCCCTCCCGGA 3293
Db 3228 GATAGTTGCGCAGACC-----GAGCGCGCGGAACCGGA 3260
Qy 3294 GCTAGACGCGCGCCCGCAGGGACGAGCCGCGCCCGCCCGAGCGCCCTGCGCTCCCGCGC 3353
Db 3261 AGCGGGTGTAGTAACACTCAATGCGGGTACGCGCCCAAAACCCCGTGTGTAACCAAGCCG 3320
Qy 3354 CAAGCGCCCGCGGAGACGCGTGCATGCGGACCCCGCGGAGCGCGTCCCAAGCCCGC 3413
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Db 3321 ACGCCCCCAACCTAA-----ACG 3338
Qy 3414 CAAAGCTGCTGGTCCGAGCTGGCGGAGGATCCCGGTACGCCATCGCCCGGGCGTTC 3473
Db 3339 CAAACTGCTGGTTTCGACCTCGCCGAAGACCCGACCTATGTTCCGAGAATGACGTACC 3398
Qy 3474 GCTCAACACGAGACTATTACTTCTCGACCTGCTGGGGGCGGCTGCGTGAAGGCTCAAGGC 3533
Db 3399 GCTAAACACAGACTACTATTCTCTCCACCTGTTGGGTACCATTAAGCGTGAACCTTTAAGGC 3458
Qy 3534 CTTGTTTGAATAAAGCCCAAGATCACCGAGAGTCTGTTAAAGAGGTTTATTCGCCGAGAC 3593
Db 3459 TCTATTTCGGAATGATGTGAGAAACAAGAAAATCTTTTAAAGCGGTTTATTCGGAAC 3518
Qy 3594 GTGGCAC---CCGCCGACGACGTGGCGCGCGCTCAGGGCGCGGGTTCGGGCGCGC 3650
Db 3519 CCCCACAAGACCCCAAGAACCCAGGACCTGCTTGAGCGCGCGCTTGAAAAGCT 3578
Qy 3651 GGGGGCGCGCTACCGCGGAGGAAACTCGTCAATGTTGTCATAGAGCCTTTGATACTCT 3710
Db 3579 GACGCCCTTACACCGGAGGAGAAAGTCTCGAATACCTGCATACAGTTTTTTTGTACTCT 3638
Qy 3711 AGCA 3714
Db 3639 AGAA 3642

RESULT 14
ADP74214/c
ID ADP74214 standard; DNA; 14411 BP.
XX
AC ADP74214;
XX
DT 26-AUG-2004 (first entry)
XX
DE Equine herpesvirus 4 genome gM deletion mutant #2.
XX
KW virucide; vaccine; Equine Herpes Virus; EHV; gM; vaccine;
KW EHV-associated condition; Equine herpesvirus 4; EHV4; ds; mutant; mutein.
XX
OS Equine herpesvirus 4.
OS Synthetic.
XX
US2004109873-A1.
XX
PD 10-JUN-2004.
XX
PF 21-JUL-2003; 2003US-00624149.
XX
PR 19-JUL-2002; 2002DE-01033064.
PR 14-AUG-2002; 2002US-0403282P.
PR 11-APR-2003; 2003DE-01017008.
XX
PA (BOEH ) BOEHRINGER INGELHEIM VETMEDICA GMBH.
XX
PI Neubauer A, Ziegler C;
XX
WIPI; 2004-440311/41.
XX
PT New recombinant equine herpes (EHV) virus free of heterologous elements,
PT and where protein gM has been deleted, useful as a vaccine for treating
PT or preventing EHV infections.
XX
PS Claim 18; Page; 156pp; English.
XX
CC The invention describes a new recombinant Equine Herpes Virus (EHV) where
CC the protein gM is absent, and the EHV is free of heterologous elements.
CC Also described are: a nucleic acid coding for an EHV defined above; a
CC vaccine preparation comprising the EHV or nucleic acid; obtaining a
CC recombinant EHV; and a cell line for use in the method, where the gene
CC encoding the protein gM is transfected into the cell line, and the cell
CC line expresses gM. The vaccine comprising the EHV or nucleic acid
CC encoding EHV is useful for treating and/or preventing EHV-associated
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CC condition, and for monitoring the therapeutic success. The recombinant  
CC EHV is useful as a vaccine against EHV infections. This sequence  
CC represents an Equine herpesvirus 4 genome in which nucleotides 92681-  
CC 93865, comprising regions of the gM gene, have been deleted.

Query Match	23.8%	Score 885.8	DB 12	Length 144411	
Best Local Similarity	55.2%	Pred. No. 3.9e-134			
Matches 1986	Conservative	0	Mismatches 1452	Indels 159	Gaps 7
Qy	193	CGCCATACGTACTACAGCGAGTGCAGCAAGTATTCGATTTATCGCCCCGGTTCGCTGCAC	252		
Db	54794	CACCACTCATCTACACCGAGGTGGCACTTCAAGTTCTATAGCACCCAGTGTCTTGAT	54735		
Qy	253	GAGAGCCGCCCGCGGAGCAGCGCACCGGGTCCACGACGGCGGCTCCGGCGCGCCCT	312		
Db	54734	GAAGATGCTCCAAACCGATCAGCGACGCGTGTGCATGTGGGAACACTTTGAGCGCACCCCA	54675		
Qy	313	AAGGTGTACTCGCGGGGACAGCGCGACGCTCTCCGGTGGGCCCGGAGGGCTTCGG	372		
Db	54674	AAAGTGTACTGTGATGGCGCAGAGTACGACGCTCTAGACTTTGAAGCTGACGCTTGTGCG	54615		
Qy	373	CCGCGTGCCTTGGCGCTGTGGGCGGTGGGACCATGCCCCCAAGGGGTTCGACCCAC	432		
Db	54614	CCTCGCAGGATTCCGGTTTGGAAACGCAAGATTTTCGGGTGATGAGTTTAAACCAAGA	54555		
Qy	433	GTCAACGCTCTTCACGCTACGACATCTCTGGAGCAGCTGGAAACACGCGTACAGCATGGC	492		
Db	54554	TTTGAGAGGTTTCACTGTACGACATAGTAGAGTTTGTGGAAAGCGCTTCGAAACGACGAC	54495		
Qy	493	GCGCCCCAGCTCCACGAGCGATTTATGGACGCGCATCAGCCCGCGGACCGTATCAG	552		
Db	54494	CCGTCGCGGTTTGCCTAGCTACTCT-----CGCCCAAGCGGATCAGTGGTAACA	54447		
Qy	553	CTTCTGGGTGACCCCCGAGAGGCCATTCGCGTCGCGTTTCAGTCTACGGCACGCGGAG	612		
Db	54446	TTGCTGGGAATGAGCGAATGTGGAAAGCGCGTAGCGGTTTCAGTGTACGCTGTGCGCCAT	54387		
Qy	613	TACTTTTACATGAACAAAGCGGAGTGGATCG-GCACCTGCACTGCCGTGCCCGCGCGA	671		
Db	54386	TATTTTATATTGAAAGTCAAGATGAGACAGAGCGTGTGGNATAACAGAGCATCCGAC	54327		
Qy	672	TCTCTCGAGAGCGCTCGCGCGGCGCTTCGCGAGTGC CGGGGGCGTCTGTTCCGCGCAT	731		
Db	54326	CTAGTTTCGCGCCATGTTTCCTCGCGCATAACTCAGCTTTTAAAGCGCGCTCGGAAAT	54267		
Qy	732	CTCCGCGGACCACTTCGAGCGGAGTGTGTGAGCGCGCGCAGC-----	775		
Db	54266	AGCAACGAGGAAACAAAGCGGTGAAACAGCGCGGCTGTGTGGGAGGAAAGCAGTA	54207		
Qy	776	-----TGACTATTACGAAACG	792		
Db	54206	TCTCTGATGCTTTTAAAGTTGAAACAGTATGCCACACAGCGCTGTACTATTGGATCA	54147		
Qy	793	CGCCGACCTGTACTACCGCTCTTCGTGCGAAGGGCGCGCTGCTACTCTGTGC	852		
Db	54146	AAGCCAAACCTCTACTATAGGGTTTCATCCTCTAGAGTGCCTGTGGCGGGTTTATCTGC	54087		
Qy	853	GACAACTTTTGGCCCCGCTACGGAAGTACGAGGGGGCGTTCGACGCCACACCCCGGTTT	912		
Db	54086	GATAACTTCCACCGGAAATCACAAAATTTGAGGGGAGTGTGGATGTAAACACGCGCTC	54027		
Qy	913	ATCCTGGACAAACCGGGGTTTGTCACTTCGCTGTTACCGCTCAAGCCCGCGCGGG	972		
Db	54026	TTGTTGGACAATGAAATTTTACCAAGTTTGGGTGGTACCGCTCCGCGCGGAAACAA	53967		
Qy	973	AACGCGCGCGCCAAACCGCGCCCCCGACGCGGTTTCGAAACCTCGAGCGAGCTCGAGTTT	1032		
Db	53966	GGAGAGCGTGTCACTGCGCCAGGTGAGCGACACCTGACCTCAAGTACGTTGAAAT	53907		
Qy	1033	AACCTCACCGCGGACAACTCTGCGCGTTCGAGGGGGCCATGTGTGACCTGCGCGCTCAAG	1092		

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QY 2161 TTTGCCAGCTGTACCCAGCATCATCCAGGCCACAACTGTGCTTCAGTACGCTCTCC 2220
|||
Db 52766 TTTGGAGCTGTATCCAGCATCATCCAGGCCACAACTTTGTTTCACCACTTAGCC 52707
|||
QY 2221 CTGCGGCCGAGGCGCTCGGCACCTCGGAGCGGACCGGAGCTACTCTGGAGATCGAGGTG 2280
|||
Db 52706 CTTAAATGAAGTGGATTTGGCTGGGCTTCAGCCGCTGTCTTCACTACTCAACGTTTGAGGTG 52647
|||
QY 2281 GGGGGCCGACGGCTGTCTTCGTGAAGGCCCACTAGCCGAGAGCCCTGCTGAGATCCTG 2340
|||
Db 52646 GGGGACCAAAAGTTGTTTTTGTGTCACGCGCACTTCGCGAAAAGCTTGCTTGTAFTTTG 52587
|||
QY 2341 CTGCGGACCTGGCTGGCCATCGGAAAGCAGATCCGCTCGCGGATCCGCCAGAGCACCC 2400
|||
Db 52586 CTGCGGACCTGGCTGGCTATGCGAAAGCTGTAGGCGAGATTCGAAAGTAAATGCAACTCA 52527
|||
QY 2401 GAGGAGCGCTGCTCTCTCGAAGCAACAGGCCGCCATCAAGGTGGTGTGCAACTCGGTG 2460
|||
Db 52526 GAGGAGCGAGTTTGTCTAGATAAGCAACAGCTCTGCAATTAAGTAATATGCAACTCA 52467
|||
QY 2461 TAGGGTTACCGGGGCGAGCAGCGTCTTCTGCCCCCTGCGACGCTGGCGCGCACCGTG 2520
|||
Db 52466 TAGCGATTACCGGCTGTGGCAACCGGACTGTGTCATTTGAGAAATAGCAGCCCGTT 52407
|||
QY 2521 ACGACCATCGCGCGAGATGCTCTCTCGCAGCGCGCGCTACGTGCAACGCGCTGGGCG 2580
|||
Db 52406 ACTACAATAGCCGCAACATGCTCTCAAAACGAGAGATTACGTTCACTATCTGTTGGGCG 52347
|||
QY 2581 GAGTTCCATCAGTGTGCGCGACTTTCCGAGCGCGCCGCGCATGCGCGCCCCCGGTCCG 2640
|||
Db 52346 ACGCGTGAGCTGTTGGAAAACAACTCCAGGGGCTTTAAATTTTCGCAACAAAGCC 52287
|||
QY 2641 TACTCCATGGCATCATCTAGGGGACACGGACTCCATTTTGTGTCGCGGCGCTC 2700
|||
Db 52286 TATTCTGTACAGAGTTATTACCGGAGACACCGACTCTGTATTCATCAAGTTTGTGGGCTA 52227
|||
QY 2701 ACGCGCGCGGCTGTGGCCATCGGCGCAAAAGATGCGAGCCACATCTCGCGCGCTG 2760
|||
Db 52226 ACATACAGGGGTTTCAGAGCTTGGAGATTCATGTTCGCGACAGATTCAGCTGACCTT 52167
|||
QY 2761 TTCCTCCCGGATCAAGCTCGAGTGGAGCGGAAAAAGTTTCAACAGCTGTGCTCATCGCC 2820
|||
Db 52166 TTTAAAGCACCTATCAAACTAGAGTGTGAAAAACCTTCCAGCGCTGCTACTAAATPACA 52107
|||
QY 2821 AAGAAAAGTACATCGGCTCATCTCGGGGGCAAGATGCTCATCAAGGGGCTGGATCTG 2880
|||
Db 52106 AAGAAAAGTACATAGGTGTATCAACGGGGGTATATGTCTCATGAAGGGGGTAGACCTA 52047
|||
QY 2881 GTGCGCAAAACAACTGCGCGTTTATCAACCGCACCTCCAGGGGCTTGGTTCGACCTGCTG 2940
|||
Db 52046 GTCCGTAAATAAATACTGTGCTTCATATACTTCTACGGGACATCTAGTAGATCTTCTG 51987
|||
QY 2941 TTTTACGACGATACCGTATCCGAGCGCGCCGCGTTAGCCGAGCGCCCGCGACAGAGAG 3000
|||
Db 51986 TTGTACGACGAGGAGTACGTACCGCGCGCGGAGGTAACTAACGTGCTCTCCCTCAGAG 51927
|||
QY 3001 TGGCTGGCGGACCCCTGCCGAGGAGTACGAGCGCTTCGGGGCGCTCTCGTAGAGCC 3060
|||
Db 51926 TGGGTGGCGGCCCCCTTCCGAGCGGCTTTGACAAAGTTTGAAGAGTGTGTATAGAGCT 51867
|||
QY 3061 CATCGGCGCATCACCGACCCCGAGAGGAGACATCCAGGACTTTGTCCTCACCGCGCAACTG 3120
|||
Db 51866 TACAACGCTATAACCGCACCAACTTGGATGTGCGCGAGTTTGTGATGACGTCTGAGCTT 51807
|||
QY 3121 AGCAGACACCGCGCGGCTACACCAACAGGCGCTGGCCCACTGACGCGTGTATTAAG 3180
|||
Db 51806 AGCCGACCGCGGGAATCATATACAAACAAAGCGGCTACCGCACCTCACTGTTTACTTTAAG 51747
|||
QY 3181 CTCATGGCGCGCGCGAGTCCGCTCCATCAAGGACCGGATCCCGTACGTGATCGTG 3240
|||
Db 51746 CTCGCTATGCGGAATGAAGAACTGCCAGTGTGAAGGAGAGAAATTCGATATGTATGTT 51687
|||

RESULT 15
ADP74215/c
ID ADP74215 standard; DNA; 144486 BP.
XX
AC ADP74215;
XX
XX 26-AUG-2004 (first entry)
XX
DE Equine herpesvirus 4 genome gM deletion mutant #3.
XX
XX virucide; vaccine; Equine Herpes Virus; EHV; gM; vaccine;
KW EHV-associated condition; Equine herpesvirus 4; EHV4; ds; mutant; mutuin.
XX
OS Equine herpesvirus 4.
OS Synthetic.
XX
XX US2004109873-A1.
XX
XX 10-JUN-2004.
XX
XX 21-JUL-2003; 2003US-00624149.
XX
XX 19-JUL-2002; 2002DE-01033064.
XX 14-AUG-2002; 2002US-0403282P.
XX 11-APR-2003; 2003DE-01017008.
XX
XX (BOEH ) BOEHRINGER INGELHEIM VETMEDICA GMBH.
XX
XX Neubauer A, Ziegler C;
XX WPI; 2004-440311/41.
XX
XX New recombinant equine herpes (EHV) virus free of heterologous elements,
XX and where protein gM has been deleted, useful as a vaccine for treating
XX or preventing EHV infections.
XX
XX Claim 19; Page; 156pp; English.
XX
XX The invention describes a new recombinant Equine Herpes Virus (EHV) where
XX the protein gM is absent, and the EHV is free of heterologous elements.
CC
```

CC Also described are: a nucleic acid coding for an EHV defined above; a  
CC vaccine preparation comprising the EHV or nucleic acid; obtaining a  
CC recombinant EHV; and a cell line for use in the method, where the gene  
CC encoding the protein gm is transfected into the cell line, and the cell  
CC line expresses gm. The vaccine comprising the EHV or nucleic acid  
CC encoding EHV is useful for treating and/or preventing EHV-associated  
CC condition, and for monitoring the therapeutic success. The recombinant  
CC EHV is useful as a vaccine against EHV infections. This sequence  
CC represents an Equine herpesvirus 4 genome in which nucleotides 92715-  
CC 93824, comprising regions of the gm gene, have been deleted.  
XX  
SQ Sequence 144486 BP; 35916 A; 36662 C; 36259 G; 35649 T; 0 U; 0 Other;

Query Match 23.8%; Score 885.8; DB 12; Length 144486;  
Best Local Similarity 55.2%; Pred. No. 3.9e-134;  
Matches 1986; Conservative 0; Mismatches 1452; Indels 159; Gaps 7;  
QY 193 CGCCATAGCTACTACAGCGAGTGCACGAATTTTCGATTTTCGCCGCCCGTTCGCTGCAC 252  
DB 54794 CACCACTCATACTACACCGAGGTGGGCAACTTCAAGTTTCATAGCACCAAGTGTCTTGAT 54735  
QY 253 GAGGACGCCCGCGGAGCAGCGCACCGGGTCCACGACGCGCGCTCCGCGCGCCCT 312  
DB 54734 GAAGATGCTCAACCGATACGCGAGCGCGCTGTGCATGTGGAAACACTTGAGCGCACCCCA 54675  
QY 313 AAGGTGTACTCGGGGGGAGCAGCGCGACGTCCTCCCGTGGGCGCGAGGGCTTCTGG 372  
DB 54674 AAAGTGTACTGTGTGGCGCAGAGTACGACGCTCTAGACTTTGAAGCTGACGGTGTCTGG 54615  
QY 373 CGCGTCTGCTGGCGCTGTGGGCGGTGCGGACCATGCCCGCAAGGGTTCGACCCAC 432  
DB 54614 CCTCGCAGGATTCGGGGTTTGAACCGGCAAGATTTTCGCGGTGTAGTTTAAACCCAGA 54555  
QY 433 GTCACCGCTTCCACGCTGTACACATCTGTGAGCAGCTGGAAACAGCGGTACAGATGCG 492  
DB 54554 TTTGAGAGTTTACGCTGTACACATAGTAGAGTTTGTGGAAAGCGCTTCGAAACGAC 54495  
QY 493 GCCGCCAGCTCCACGAGCGATTTATGGACGCCATCACGCCCGCGCGGACCGTTCACG 552  
DB 54494 CCGTCGCGGTTTGTGAGCTATCT-----CGCCCAAGCGGATCAGTGTAA 54447  
QY 553 CTTCTGGGTCTGACCCCGAAGGCCATCGCGTCCGCTTACGCTTACGGACCGCGGAG 612  
DB 54446 TTGCTGGGAATGAGCGAATGTGGAAGCGCTAGCGGTTCACGTGTACGGTGTGCGCAT 54387  
QY 613 TACTTTTACATGAACAAGCGGAGTGTGATCG-GCACCTGAGTGCCTGCGCGCGA 671  
DB 54386 TATTTTATATTTGAAGTCAAGATGACAGAGCGTGTGGAATAACAGCGAATCCGAC 54327  
QY 672 TCTCTGAGCGCCTGGCGGCGGCCCTGCGCGAGTTCGCGGGGCGTGTTCGCGCGCAT 731  
DB 54326 CTAGTTGCGGCATGTTGCTGCGCGCATTAACCTCAGCTTTAAGGCGCGCCTCGGAAT 54267  
QY 732 CTCGCGGACCACTTCGAGGCGGAGTGTGAGCGCGCGCGAAG-----775  
DB 54266 AGCAACGAGGAGAAACAAGCGGTGGAACAAGCGCGCGCTGTGGGAGGAAGACAGTA 54207  
QY 776 -----TGTAATAATAGCAACG 792  
DB 54206 TCTCTGATTTGCTTAAAGTTGAACAGTATGCCACACGACGCTGTACTTTGGATCA 54147  
QY 793 CGCCGAGCCCTGTACTACCGCGTCTTCGTGCGAAGCGCGCGCTGGCTTACCTGTGC 852  
DB 54146 AAGCAACCTCTACTATAGGTTTTCATCTCTAGCAGTGCCTTGGGGGGTTCATCTGC 54087  
QY 853 GACAACTTTTCCCGCGCATCAGGAAGTACGAGGGGGCGTTCGACCGCAACACCCCGTTT 912  
DB 54086 GATAACTTTCCACCGGAAATCACAATAATTTGAGGGGAGTGTGGATGTAAACAACCGCGCTC 54027  
QY 913 ATCTGGACAAACCCGGGTTTGTACACCTTCGCTGTGTACCGCTTCAGCGCGCGCGGG 972  
DB 54026 TTGTTGGAATGAAATTTTACCAAGTTTGGGTGGTACCGCTTCCCGCGCGGAACCAAC 53967

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Search completed: August 6, 2005, 02:16:55  
Job time : 1891 secs





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421	Db		TTTGACCCCAACCGTACACCGTCTTCCACGTTGTAGACATCTTGGAGCAGCTGGGAACACGCG	480
481	Qy		TACAGCATGGCGCGCGGCCAGCTCCACGAGCGATTTATGGACGCCATCACGCCCGCGCGG	540
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601	Qy		GGCAGCGGGCAGTACTTTTATCATGAACAAGCGCGAGGTGATCGGCACCTGCAGTCCCGT	660
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; APPLICANT: Homa, Fred  
; APPLICANT: Wathen, Michael  
; APPLICANT: Hopkins, Todd  
; APPLICANT: Thomsen, Darrell  
; TITLE OF INVENTION: A Method for Treating Herpes Virus  
; FILE REFERENCE: 00221  
; CURRENT APPLICATION NUMBER: US/09/904,065  
; CURRENT FILING DATE: 2001-07-12  
; NUMBER OF SEQ ID NOS: 19  
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DB 421 TTGAGCCCCACCGCTCACCCTTCTCCACGTGTACGATCTCTGGAGACGCTGGAGAACGCG 480  
QY 481 TACAGATGCGCGCGCCCGAGCTCCACGAGCGATTTATGAGCGCATATGCGCCCGCGGG 540  
DB 481 TACAGATGCGCGCGCCCGAGCTCCACGAGCGATTTATGAGCGCATATGCGCCCGCGGG 540  
QY 541 ACCGTCATCACTGCTGCGTCTGAGCCCCGAGGCGCATCGCGTCCCGCTTCACTGCTAC 600  
DB 541 ACCGTCATCACTGCTGCGTCTGAGCCCCGAGGCGCATCGCGTCCCGCTTCACTGCTAC 600  
QY 601 GCGACGCGGAGTACTTTTATCATGAACAAAGCGGAGTGCATCGGCACTGCAAGTCCGT 660  
DB 601 GCGACGCGGAGTACTTTTATCATGAACAAAGCGGAGTGCATCGGCACTGCAAGTCCGT 660



2821 ATCCCAAGAAAGTATCATCGCGTCATCTGGGGGCAAGATGCTCATCAAGGGCGTG 2880  
2875 GATCTGGTGGCAAAACAACTCGCGTTTATCAACCGCACTCCAGGGCCCTGCTGCAC 2934  
2881 GATCTGGTGGCAAAACAACTCGCGTTTATCAACCGCACTCCAGGGCCCTGCTGCAC 2940  
2935 CTGCTGTTTTCAGACGATACCGTATCCGAGCGCGCCCGCTTAGCCGAGCGCCCGCA 2994  
2941 CTGCTGTTTTCAGACGATACCGTATCCGAGCGCGCCCGCTTAGCCGAGCGCCCGCA 3000  
2995 GAGGAGTGGTGGCGGACCCCTCGCCGAGGAGTGCAGCGCTTCGGGGCCCTCTCGTA 3054  
3001 GAGGAGTGGTGGCGGACCCCTCGCCGAGGAGTGCAGCGCTTCGGGGCCCTCTCGTA 3060  
3055 GAGGCCCATCGCGCATACCGACCGGAGGAGGACATCCAGGACTTTGCTTCACCGCC 3114  
3061 GAGGCCCATCGCGCATACCGACCGGAGGAGGACATCCAGGACTTTGCTTCACCGCC 3120  
3115 GAATGAGCAGACACCGCGCGGTATACCAACAAAGCGCTTGGCCCACTGACGCTGTAT 3174  
3121 GAATGAGCAGACACCGCGCGGTATACCAACAAAGCGCTTGGCCCACTGACGCTGTAT 3180  
3175 TACAAGCTCATGGCGCGCGCGAGTCCCGTCCATCAAGGACCGGATCCCGTACGTTG 3234  
3181 TACAAGCTCATGGCGCGCGCGAGTCCCGTCCATCAAGGACCGGATCCCGTACGTTG 3240  
3235 ATGCTGCGCCAGACCGCGAGGTAGAGGAGCGGTGCGCGGTGCGCGCGCTCCCGAG 3294  
3241 ATGCTGCGCCAGACCGCGAGGTAGAGGAGCGGTGCGCGGTGCGCGCGCTCCCGAG 3300  
3295 CTAGAGCGCGCGCCCGAGGAGCGAGCGCGCGCGCGCGCTTGCCTCCCGCGCC 3354  
3301 CTAGAGCGCGCGCGCGAGGAGCGCGCGCGCGCGCGCTTGCCTCCCGCGCC 3360  
3355 AAGCGCGCGCGAGAGCGCGTGCATGCGGACCGCGCGCGCGCGCGCTTGCCTCCCGCGCC 3414  
3361 AAGCGCGCGCGAGAGCGCGTGCATGCGGAGCGCGCGCGCGCGCTTGCCTCCCGCGCC 3420  
3415 AAGCTGCTGTGTCGAGCTGGCGGAGGATCCCGGATAGCCATCCCGCGCGCGCTTCCG 3474  
3421 AAGCTGCTGTGTCGAGCTGGCGGAGGATCCCGGATAGCCATCCCGCGCGCGCTTCCG 3480  
3475 CTCACACGAGCTATTACTTCTCGACCTGCTGGGGCGCGCTGCGTGAGCTTCAAGGCC 3534  
3481 CTCACACGAGCTATTACTTCTCGACCTGCTGGGGCGCGCTGCGTGAGCTTCAAGGCC 3540  
3535 CTGTTTGGAAATAACCGCAAGATCACCGAGTCTGTTAAAGAGTTTATTCGCGAGCG 3594  
3541 CTGTTTGGAAATAACCGCAAGATCACCGAGTCTGTTAAAGAGTTTATTCGCGAGCG 3600  
3595 TGGCACCCCGGACGAGCTGGCGCGCGCTCAGGGCGCGGGTTTCGGCGCGCGGG 3654  
3601 TGGCACCCCGGACGAGCTGGCGCGCGCTCAGGGCGCGGGTTTCGGCGCGCGGG 3660  
3655 GCGCGGCTACGCGGAGGAAATCGTTCGAATTTGCGATAGAGCTTTGATCTCTAGCA 3714  
3661 GCGCGGCTACGCGGAGGAAATCGTTCGAATTTGCGATAGAGCTTTGATCTCTAGCA 3720  
3715 TGA 3717  
3721 TGA 3723

RESULT 3  
US-09-827-688-8  
; Sequence 8, Application US/09827688  
; Patent No. 6821955  
; GENERAL INFORMATION:  
; APPLICANT: ORSON, FRANK  
; APPLICANT: KINSEY, BERNA  
; APPLICANT: BHOGAL, BALBIR  
; TITLE OF INVENTION: MACROAGGREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION D

; TITLE OF INVENTION: AGENTS  
; FILE REFERENCE: P01949US1/10004014  
; CURRENT APPLICATION NUMBER: US/09/827,688  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/195,680  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 154746  
; TYPE: DNA  
; ORGANISM: HERPESVIRUS 2  
; US-09-827-688-8

Query Match 99.4%; Score 3693; DB 4; Length 154746;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 3712; Conservative 0; Mismatches 5; Indels 6; Gaps 1;  
QY 1 ATGTTTGTGCGCGCGCGCGCGCTTCCCGGGGGGAAAGTCCGGCGCTCGGGCGCGG 60  
DB 63265 ATGTTTGTGCGCGCGCGCGCGCTTCCCGGGGGGAAAGTCCGGCGCTCGGGCGCGG 63324  
QY 61 TCTGGGTTTTTTCGCCCCCAAAACCCCGGGGAGCCACCCAGACGGGACCGCCGCTTGC 120  
DB 63325 TCTGGGTTTTTTCGCCCCCAAAACCCCGGGGAGCCACCCAGACGGGACCGCCGCTTGC 63384  
QY 121 CGCGCGCAGAACTTCTACAAACCCCACTCGCTCAGACGGGACGAGCCAAAGGCCCCC 180  
DB 63385 CGCGCGCAGAACTTCTACAAACCCCACTCGCTCAGACGGGACGAGCCAAAGGCCCCC 63444  
QY 181 GGGCGCGCTCAGCGCCATACGTACTACAGCGAGTGCAGGAATTTTCGATTTATTCGCCCG 240  
DB 63445 GGGCGCGCTCAGCGCCATACGTACTACAGCGAGTGCAGGAATTTTCGATTTATTCGCCCG 63504  
QY 241 CGTTCGCTGGAAGAGACCGCCCGCGGAGAGCGCAACCGGGTCCAGACGGCGCGCTC 300  
DB 63505 CGTTCGCTGGAAGAGACCGCCCGCGGAGAGCGCAACCGGGTCCAGACGGCGCGCTC 63564  
QY 301 CGCGCGCGCTTAAGGTGACTGCGGGGGGAGCGAGCGAGCTCTCCGCGTGGGCGCG 360  
DB 63565 CGCGCGCGCTTAAGGTGACTGCGGGGGGAGCGAGCGAGCTCTCCGCGTGGGCGCG 63624  
QY 361 GAGGGCTTTCGCGCGCTGCTTGGCGCTTGTGGGGCGTGCAGACCATGCCCCCAAGGGG 420  
DB 63625 GAGGGCTTTCGCGCGCTGCTTGGCGCTTGTGGGGCGTGCAGACCATGCCCCCAAGGGG 63684  
QY 421 TTCAGACCCACCGTCACCGCTTTCACGTTGACGATCCTGGAGACGCTGGAAACGCG 480  
DB 63685 TTCAGACCCACCGTCACCGCTTTCACGTTGACGATCCTGGAGACGCTGGAAACGCG 63744  
QY 481 TACAGCATGCGCGCGCGCGCTCCAGCGAGCTTATCGAGCGCATACGCCCGCGCGG 540  
DB 63745 TACAGCATGCGCGCGCGCGCTCCAGCGAGCTTATCGAGCGCATACGCCCGCGCGG 63804  
QY 541 ACCGTCATCACGCTTCTGGGTCTGACCCCGAAGGCATCGGCTCGCGCTTCACTGCTAC 600  
DB 63805 ACCGTCATCACGCTTCTGGGTCTGACCCCGAAGGCATCGGCTCGCGCTTCACTGCTAC 63864  
QY 601 GGCAGCGCGCAGTACTTTTACATGAACAAAGGGGAGGTGGATCGGCACTGCAAGTCCCGT 660  
DB 63865 GGCAGCGCGCAGTACTTTTACATGAACAAAGGGGAGGTGGATCGGCACTGCAAGTCCCGT 63924  
QY 661 GCCCGCGCGATCTCGGAGCGCTTGGCGGGCGCTTGGCGAGTTCGCCGGGGGCGTGC 720  
DB 63925 GCCCGCGCGATCTCTCGGAGCGCTTGGCGGGCGCTTGGCGAGTTCGCCGGGGGCGTGC 63984  
QY 721 TTTCGCGCATCTCCGCGGACCACTTTCGAGGGCGAGGTGGTGGAGCGCGCCGACGCTGAT 780  
DB 63985 TTTCGCGCATCTCCGCGGACCACTTTCGAGGGCGAGGTGGTGGAGCGCGCCGACGCTGAT 64044  
QY 781 TATTACGAAACCGCGCGGACCTGTACTACCGCGTCTTCGTGCGAAGCGGGCGCGCGCTG 840  
DB 64045 TATTACGAAACCGCGCGGACCTGTACTACCGCGTCTTCGTGCGAAGCGGGCGCGCGCTG 64104



QY	841	GCCTACCTGTGCGACAACTTTTGC	CCCGCGGATCAGGAAGTACGAGGGGGCGGTTCGACGCC	900	1921	CAGGGGCGGTTTTCGGGGCCTTCGA	CAAGGAGCGGCCCAAGCGCCCGCGTGCCTTCGGGG	1980	
Db	64105	GCCTACCTGTGCGACAACTTTTGC	CCCGCGGATCAGGAAGTACGAGGGGGCGGTTCGACGCC	64164	65185	CAGGGGCGGTTTTCGGGGCCTTCGA	CAAGGAGCGGCCCAAGCGCCCGCGCGTGCCTTCGGGG	65244	
QY	901	ACCAACCGGTTTATCTTGGA	CAACCCGGGGTTTGTCACTTCGGCTGGTGTACCGCTCAAG	960	1981	GAAGGGAGCGCGCGGGGACGGGA	ACGGGACAGGATTAAGGACGACACGA-----G	2034	
Db	64165	ACCAACCGGTTTATCTTGGA	CAACCCGGGGTTTGTCACTTCGGCTGGTGTACCGCTCAAG	64224	65245	GAAGGGAGCGCGCGGGGACGGGA	ACGGGACAGGATTAAGGACGACGACGAGGACGG	65304	
QY	961	CCGGCGCGGGGAAACGCGCGG	CCCAACCGCGCCCCCGACCGCGTTCGGAACTTCGAGC	1020	2035	GAAGGACGCGGGGACGAGCGCG	GAGGTCGCGCGGAGACCGGGGGCCCGGACCGTTGGG	2094	
Db	64225	CCGGCGCGGGGAAACGCGCGG	CCCAACCGCGCCCCCGACCGCGTTCGGAACTTCGAGC	64284	65305	GACGAGACCGGGACGAGACGCG	GAGGTCGCGCGGAGACCGGGGGCCCGGACCGTTGGG	65364	
QY	1021	GAGCTCGAGTTTAACTGCA	CGCGGACAACTTGCCGTCGAGGGGGCCATGTGTGACCTG	1080	2095	TACCAGGGGGCCCGGGTCTTCG	ACCCACCTTCGGGGTTTCAAGTCGACCCCGTGGTGGTG	2154	
Db	64285	GAGCTCGAGTTTAACTGCA	CGCGGACAACTTGCCGTCGAGGGGGCCATGTGTGACCTG	64344	65365	TACCAGGGGGCCCGGGTCTTCG	ACCCACCTTCGGGGTTTCAAGTCGACCCCGTGGTGGTG	65424	
QY	1081	CGGGCTTACAAGCTCATGTG	CTTCGATATCGAATGCAAGCGGGGGGAGGACGAGCTG	1140	2155	TTTGTACTTTGCCAGCTGTAT	ACCCAGCATCATCCAGGCCCAACCTGTGCTTCAGTPAG	2214	
Db	64345	CGGGCTTACAAGCTCATGTG	CTTCGATATCGAATGCAAGCGGGGGGAGGACGAGCTG	64404	65425	TTTGTACTTTGCCAGCTGTAT	ACCCAGCATCATCCAGGCCCAACCTGTGCTTCAGTPAG	65484	
QY	1141	GCCTTTCGGGTCCGGAAG	CGCCCGGAAGACCTGCTCATCCAGATCTCTGTCTGTCTTAC	1200	2215	CTCTCCCTGCGGCCCGGAGG	CGCTCGCACCTCGAGGCGGACCGGGACATACCTGGAGATC	2274	
Db	64405	GCCTTTCGGGTCCGGAAG	CGCCCGGAAGACCTGCTCATCCAGATCTCTGTCTGTCTTAC	64464	65485	CTCTCCCTGCGGCCCGGAGG	CGCTCGCACCTCGAGGCGGACCGGGACATACCTGGAGATC	65544	
QY	1201	GACTGTGCCACACCGCCCT	CGACACATCTCTCTGTTTTCGCTCGGATCTTCGACCTC	1260	2275	GAGGTGGGGGGCCGACCGGCT	GTCTTCGTGAAGGCCCACTGACGCGAGAGCCCTGCTGAGC	2334	
Db	64465	GACTGTGCCACACCGCCCT	CGACACATCTCTCTGTTTTCGCTCGGATCTTCGACCTC	64524	65545	GAGGTGGGGGGCCGACCGGCT	GTCTTCGTGAAGGCCCACTGACGCGAGAGCCCTGCTGAGC	65604	
QY	1261	CCGAGTCCCACTCAGCGAT	CTCGCCTCCAGGGGCGCTCGCGCCCGCTCGTCTCTGGAG	1320	2335	ATCTCTGCTGCGGATCGGCT	GTGCGCATGCGAAAGAGATCTCGCTCGCGGATCTCCCGCAGAGC	2394	
Db	64525	CCGAGTCCCACTCAGCGAT	CTCGCCTCCAGGGGCGCTCGCGCCCGCTCGTCTCTGGAG	64584	65605	ATCTCTGCTGCGGATCGGCT	GTGCGCATGCGAAAGAGATCTCGCTCGCGGATCTCCCGCAGAGC	65664	
QY	1321	TTTGA	CAGCGAAATTCAGATGTCTG	CTGGCTTCATGACCTTTCGTCAAGCAGTACGGCCCC	2454	2395	ACCCCGGAGGAGGCGCTCTCT	CGACAAGCAACAGGCGCCCATCAAGGTGGTGTGCAAC	2454
Db	64585	TTTGA	CAGCGAAATTCAGATGTCTG	CTGGCTTCATGACCTTTCGTCAAGCAGTACGGCCCC	64644	65665	ACCCCGGAGGAGGCGCTCTCT	CGACAAGCAACAGGCGCCCATCAAGGTGGTGTGCAAC	65724
QY	1381	GAGTTGCTGACCGGGTAC	AAACATCATCACTTCGAGCTGGCCCTTCGTCTGACCAAGCTG	1440	2455	TCGGTGTACCGGTTTCA	CCCGGGCGCGACACGGGTCTTCGTGCGCTTCGTGCAAGCTGGCGCGC	2514	
Db	64645	GAGTTGCTGACCGGGTAC	AAACATCATCACTTCGAGCTGGCCCTTCGTCTGACCAAGCTG	64704	65725	TCGGTGTACCGGTTTCA	CCCGGGGTGCGACACGGGTCTTCGTGCGCTTCGTGCAAGCTGGCGCGC	65784	
QY	1441	ACGGAGATCTCAAGGT	CCCGCTCGACGGGTACGGCGCGCATGAA	CGGCGGGGTGTGTTTC	2515	ACCGTGACGACCAATCGGCG	CGCGAGATGTCTCTCGCACGCGCGGTACGTTGCAAGCGCGC	2574	
Db	64705	ACGGAGATCTCAAGGT	CCCGCTCGACGGGTACGGCGCGCATGAA	CGGCGGGGTGTGTTTC	65785	ACCGTGACGACCAATCGGCG	CGCGAGATGTCTCTCGCACGCGCGGTACGTTGCAAGCGCGC	65844	
QY	1501	CGCGTGTGGACATCGG	CCAGAGCCACTTTTCAAGCGCAGCAAGATCAAGGTGAAACGGG	1560	2575	TGGCGGAGTTTCGATAGCT	GTCTGCGGCGACTTTTCGAGGCGCGCGCATGCGCGCCCC	2634	
Db	64765	CGCGTGTGGACATCGG	CCAGAGCCACTTTTCAAGCGCAGCAAGATCAAGGTGAAACGGG	64824	65845	TGGCGGAGTTTCGATAGCT	GTCTGCGGCGACTTTTCGAGGCGCGCGCATGCGCGCCCC	65904	
QY	1561	ATGGTGAAATCGACAT	GTACGGCATATCACCGAACAGGTCAAACTCTCCAGCTACAG	1620	2635	GCTCCGTACTCCATGCG	CATCTACGGGACACGGGATCTCAATTTGTTTGTGCGCG	2694	
Db	64825	ATGGTGAAATCGACAT	GTACGGCATATCACCGAACAGGTCAAACTCTCCAGCTACAG	64884	65905	GGTCCGTACTCCATGCG	CATCTACGGGACACGGGATCTCAATTTGTTTGTGCGCG	65964	
QY	1621	CTGAACCGCGTCCCGAG	GGCGGCTTTGAAGGACAAAGAAAGGATCTGAGCTACCGGAC	1680	2695	GGCTCTACCGGCGCGGCT	GTGGCCATGCGGCGCAAAAGATGCGAGCCACATCTCGCGC	2754	
Db	64885	CTGAACCGCGTCCCGAG	GGCGGCTTTGAAGGACAAAGAAAGGATCTGAGCTACCGGAC	64944	65965	GGCTCTACCGGCGCGGCT	GTGGCCATGCGGCGCAAAAGATGCGAGCCACATCTCGCGC	66024	
QY	1681	ATCCCGCCTACTACGC	CTCCGGGCCCGCGAGCGGGGTGATCGGCGAGTATTGTGTG	1740	2755	GGCTGTGTTCTCTCCCC	CGATCAAGCTCGAATAAAAAAGTTTACCAAGCTGCTGCTC	2814	
Db	64945	ATCCCGCCTACTACGC	CTCCGGGCCCGCGAGCGGGGTGATCGGCGAGTATTGTGTG	65004	66025	GCGTGTGTTCTCTCCCC	CGATCAAGCTCGAATAAAAAAGTTTACCAAGCTGCTGCTC	66084	
QY	1741	CAGGACTCGCTGTGTC	GGGAGCTGTTCTTCAAGTTTCTGCGGACCTGGAGCTTTCC	1800	2815	ATCGCCAAAGAAAAAGT	ATACATCGGCGTCTCTGCGGGGCAAGATGTCTCATCAAGGGGCGTG	2874	
Db	65005	CAGGACTCGCTGTGTC	GGGAGCTGTTCTTCAAGTTTCTGCGGACCTGGAGCTTTCC	65064	66085	ATCGCCAAAGAAAAAGT	ATACATCGGCGTCTCTGCGGGGCAAGATGTCTCATCAAGGGGCGTG	66144	
QY	1801	GCGT	CGCGCGCTTGGCGGGCAT	CAACATCACCGGACCATCTTACGACGGCCAGCAGATC	1860	2875	GATCTGTTGCGCAAAAA	CAAACTGCGCGTTTATCAACCGCACCTCCAGGGGCCCTGTTGTCAC	2934
Db	65065	GCGT	CGCGCGCTTGGCGGGCAT	CAACATCACCGGACCATCTTACGACGGCCAGCAGATC	65124	66145	GATCTGTTGCGCAAAAA	CAAACTGCGCGTTTATCAACCGCACCTCCAGGGGCCCTGTTGTCAC	66204
QY	1861	CGGT	CTTCAAGTCTCTCG	CGCTTGGGGCCAGAGGGCTTCATCTCGCGGACACC	1920	2935	CTGCTGTTTTACGAC	AGTATCCGAGCGGCGCGCTTGTAGCCGAGCGCCCCGCA	2994
Db	65125	CGGT	CTTCAAGTCTCTCG	CGCTTGGGGCCAGAGGGCTTCATCTCGCGGACACC	65184	66205	CTGCTGTTTTACGAC	AGTATCCGAGCGGCGCGCTTGTAGCCGAGCGCCCCGCA	66264
						2995	GAGGAGTGGCTGGCG	CGACCCCTGCGCGGAGGACCTGCGGCGGTTCGAGGCGCTTCCTCGTA	3054



Db 66265 GAGGAGTGGCTGGCGGACCCCTGCCGAGGGACTGCGAGGCGTTTCGGGGCGGTCTCTCGTA 66324  
Qy 3055 GAGGCCATCGCGGCATCAGGACCCGGAGAGGGACATCCAGGACTTTGTCCTCAGGCC 3114  
Db 66325 GAGGCCATCGCGGCATCAGGACCCGGAGAGGGACATCCAGGACTTTGTCCTCAGGCC 66384  
Qy 3115 GAACTGAGCAGACACCGCGCGGTACACAAACAAGCGCTTGGCCACCTGACGGGTGAT 3174  
Db 66385 GAACTGAGCAGACACCGCGCGGTACACAAACAAGCGCTTGGCCACCTGACGGGTGAT 66444  
Qy 3175 TACAAGCTATGCGCCCGCGCGAGTCCCTTCATCAAGACCGGATCCCGTACGTG 3234  
Db 66445 TACAAGCTATGCGCCCGCGCGAGTCCCTTCATCAAGACCGGATCCCGTACGTG 66504  
Qy 3235 ATGCTGCGCAGACCCGCGAGGTAGAGGAGACGGTCCGCGGCTGGCGCGCTCCCGGAG 3294  
Db 66505 ATGCTGCGCAGACCCGCGAGGTAGAGGAGACGGTCCGCGGCTGGCGCGCTCCCGGAG 66564  
Qy 3295 CTAGAGCGCGCCCGCGAGGACGACCCCGCGCGCTTGGCCACCTTCCCGGCC 3354  
Db 66565 CTAGAGCGCGCCCGCGAGGACGACCCCGCGCGCTTGGCCACCTTCCCGGCC 66624  
Qy 3355 AAGCGCCCGCGGAGACCGCTCGCATGCGGACCCCGCGGAGCGCGTCCAAAGCCCGC 3414  
Db 66625 AAGCGCCCGCGGAGACCGCTCGCATGCGGACCCCGCGGAGCGCGTCCAAAGCCCGC 66684  
Qy 3415 AAGCTGCTGCTGCGGAGTGGCGGAGGATCCCGGATCGCCATCGCCGCGGCGTTCG 3474  
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Qy 3475 CTCAACGAGACTTACTTCTCGCACCTGCTGGGGCGGCTCGTGAGCTTCAAGGCC 3534  
Db 66745 CTCAACGAGACTTACTTCTCGCACCTGCTGGGGCGGCTCGTGAGCTTCAAGGCC 66804  
Qy 3535 CTGTTTGGAAATAACGCGAGATCAACGAGTCTGTTAAAGAGTTTATTCGCGAGACG 3594  
Db 66805 CTGTTTGGAAATAACGCGAGATCAACGAGTCTGTTAAAGAGTTTATTCGCGAGACG 66864  
Qy 3595 TGGCACCCCGCGACGAGCTGGCGCGGCTCAGGGCCGCGGGTTCGGCGCGGGGG 3654  
Db 66865 TGGCACCCCGCGACGAGCTGGCGCGGCTCAGGGCCGCGGGTTCGGCGCGGGGG 66924  
Qy 3655 GCGGCGCTACGCGGAGGAACTCGTTCGAACTGTCATAGAGCTTTGATCTCTAGCA 3714  
Db 66925 GCGGCGCTACGCGGAGGAACTCGTTCGAACTGTCATAGAGCTTTGATCTCTAGCA 66984  
Qy 3715 TGA 3717  
Db 66985 TGA 66987

RESULT 4  
US-09-904-065-5  
; Sequence 5, Application US/09904065  
; Patent No. 668282  
; GENERAL INFORMATION:  
; APPLICANT: Homa, Fred  
; APPLICANT: Wathen, Michael  
; APPLICANT: Hopkins, Todd  
; APPLICANT: Thomsen, Darrell  
; TITLE OF INVENTION: A Method for Treating Herpes Virus  
; FILE REFERENCE: 00221  
; CURRENT APPLICATION NUMBER: US/09/904,065  
; CURRENT FILING DATE: 2001-07-12  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 3708  
; TYPE: DNA  
; ORGANISM: herpes simplex  
US-09-904-065-5

Query Match 82.3%; Score 3059.8; DB 4; Length 3708;  
Best Local Similarity 89.3%; Pred. No. 0;  
Matches 3321; Conservative 0; Mismatches 387; Indels 9; Gaps 2;  
Qy 1 ATGTTTGTGCGCGCGCGCGCGCGCTTCCCGGGGGAAGTCGCGGCTCGGGGCGCG 60  
Db 1 ATGTTTGTGCGCGCGCGCGCGCGCTTCCCGGGGGAAGTCGCGGCTCGGGGCGCG 60  
Qy 61 TCTGGGTTTTTTCG 120  
Db 61 TCGGGTTTTTTCG 117  
Qy 121 CGCGCGCAGAACTTCTTACAAACCCCACTCGCTCAGACCGGAAACGACGCAAGGCGCC 180  
Db 118 TTGAGGCAAACTTTTACAAACCCCACTCGCTCAGACCGGAAACGACGCAAGGCGCG 177  
Qy 181 GGGCGGCTCAGCGCATACGTA CTA CAGCGAGTGCAGCAATTTTCGATTTATCGCCCG 240  
Db 178 GGGCCAAACCGCGCATACGTA CTA CAGCGAGTGCAGCAATTTTCGATTTATCGCCCG 237  
Qy 241 CGTTGCTGAGAGGACCGCGCGGAGCGCACCGGGTCCACGACGCGCGCGCTC 300  
Db 238 CGGGTCTGAGAGGATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 297  
Qy 301 CGCGCGCGCGCTTAAAGGTGTA CTA CAGCGGAGCGCACCGGGTCCACGACGCGCG 360  
Db 298 AAGCG 357  
Qy 361 GAGGGCTTCTGCGCGCGCTCGCTTGGCGCTGTGGGCGGTGCGGACCATGCCCGCAAGGG 420  
Db 358 GCGCGCTTCTGCGCGCGCGCTCGCGCTGTGGGCGCGGTGCGACCAACGCGCGCG 417  
Qy 421 TTGCGACCCCGCGCGCGCTTCCAGCTGTA CAGCATCTTGGAGCAGCTGGAACACGCG 480  
Db 418 TTCAACCCCGCGCGCGCTTCCAGCTGTA CAGCATCTTGGAGAACCTGGAACACGCG 477  
Qy 481 TACAGCATCGCGCGCGCGCGCTTCCAGAGCGATTTATGAGCGCATCAACGCGCGCG 540  
Db 478 TACGCGATGCGCGCGCGCGCTTCCAGCGCGCTTATGAGCGCATCAACGCGCGCG 537  
Qy 541 ACCTGATCACTGCTGCGTCTGAGTCTGACCCCGGAGCGCATCGCGTCCCGCTACGCTAC 600  
Db 538 ACCGTATCACTGCTGCGGCTGACTCCGGAAGCGCACCGGCTGCGCTTACGCTTAC 597  
Qy 601 GGCACGCGCGCTTCTTACATGACAGGCGGAGTGGATCGGACCTGCGAGTCCCGT 660  
Db 598 GGCACGCGCGCTTCTTACATGACAGGAGGAGTGGATCGGAGCGCGCGCTTACAT 657  
Qy 661 GCGCGCGCGCTTCTGCGAGCGCTTGGCGCGCGCGCTGCGAGTCCGCGCGCGCGCTG 720  
Db 658 GCGCGCGCGCTTCTGCGAGCGCATGGCGCGCGCGCTGCGAGTCCCGCGCGCGCTG 717  
Qy 721 TTTCCGCGCATCTCGCGCGACCATCTTTCGAGGCGGAGTGGTGGAGCGCGCGCGCTAC 780  
Db 718 TTTCCGCGCATCTCGCGCGACCATCTTTCGAGGCGGAGTGGTGGAGCGCGCGCTAC 777  
Qy 781 TATTAGAAACGCGCGCGCTTCTTACATCGCGCTTCTGTCGAGAGCGCGCGCGCTG 840  
Db 778 TACTAGAGACGCGCGCGCTTCTGTTTTTACCGCGCTTACGTCGGAAGCGCGCGCTG 837  
Qy 841 GCTTACCTGTCGCAAACTTTTTCGCGCGGATCAGGAAGTACGAGGGGCGCTGCAAGCC 900  
Db 838 TGTACTCTGTGCAAACTTTTTCGCGCGGATCAGGAAGTACGAGGGTGGGTGCGAGCC 897  
Qy 901 ACCACCGGTTTATCTGGAACACCGGGGTTTGTACCTTCCGCTGGTACCGCTCAAG 960  
Db 898 ACCACCGGTTTATCTGGAACACCGGGGTTTGTACCTTCCGCTGGTACCGCTCAAG 957  
Qy 961 CCGCGCGCGGAAACGCGCGCGCGCGCAACCGCGCGCGCGCGCGCGCTTCCGAACTCGAGC 1020  
Db 958 CCGCGCGGAAACCAACGCTAGCCCGCGCGCGCGCGCGCTTCCGCGCATCCAGC 1017  
Qy 1021 GACGTCGAGTTTAACTGCAACGCGGCAACCTTGGCGCTGAGGGGCGCATGTGTGACCTG 1080

1018 GAGCTCGAGTTTAACTGTACGGGAGCAACCTTGGCCATCGAGGGGGGCAATGAGCGACCTA 1077  
1081 CCGGGCTTCAAGCTCATGTGCTTCGATATCGAATATGCAAGCCGGGGGGGAGAGCAGCTG 1140  
1078 CCGGCATACAAGCTCATGTGCTTCGATATCGAATATGCAAGCCGGGGGGGAGGAGCAGCTG 1137  
1141 GCCTTTCGGTTCGGGAACCGCCGGAAGACTCTGTCATCCAGATCTCTGTGCTCTAC 1200  
1138 GCCTTTCGGTTCGGGGGACCCGAGGACCTGGTATTCAGATATCTCTGTCTCTAC 1197  
1201 GACCTGTCCACACCGCCCTCGAGACATCTCTCTGTTTTCGCTCGGATCTCTCGACCTC 1260  
1198 GACCTGTCCACACCGCCCTCGAGACATCTCTCTGTTTTCGCTCGGATCTCTCGACCTC 1257  
1261 CCGGAGTCCCACTCAGCGATCTCGCTCCAGGGGCTGCGGGCCCGTCTCTCTGAG 1320  
1258 CCGGAATCCCACTGAAAGAGCTGGCGGACAGGGGCTGCCACAGCCCGTGTCTGGAA 1317  
1321 TTTGACAGGGAATTCGAGATGCTGTGGCTTCATGACCTTCGTCAAGCATACGGCCCC 1380  
1318 TTTGACAGGGAATTCGAGATGCTGTGGCTTCATGACCTTCGTCAAGCATACGGCCCC 1377  
1381 GAGTTCTGACCGGGTACAACATCATCAACTTCGACTGGCCCTTCGTCTCTGACCAAGCTG 1440  
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				QY	3121	AGCAGACACCGCGCGCGGTACACCAAGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT	3180

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## RESULT 6

US-09-904-065-7

; Sequence 7, Application US/09904065

; Patent No. 6682892

; GENERAL INFORMATION:

; APPLICANT: Homa, Fred

; APPLICANT: Mathen, Michael

; APPLICANT: Hopkins, Todd

; APPLICANT: Thomsen, Darrell

; TITLE OF INVENTION: A Method for Treating Herpes Virus

; FILE REFERENCE: 00221

; CURRENT APPLICATION NUMBER: US/09/904,065

; CURRENT FILING DATE: 2001-07-12

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 7

; LENGTH: 3708

; TYPE: DNA

; ORGANISM: herpes simplex

US-09-904-065-7

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Query Match 82.1%; Score 3053.4; DB 4; Length 3708;
Best Local Similarity 89.2%; Pred. No. 0;
Matches 3317; Conservative 0; Mismatches 391; Indels 9; Gaps 2;
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Db 2392 GAGGAGCGGCTCTCTCTCGAACAGCAAGCGCGGCATCAAGGTGCTGTGAACTCGGTT 2451  
Qy 2461 TACGGTTTACCGGGCGCAGCACGCTCTCTGCGCTCTGCAAGTGGCGCCACCGTG 2520  
Db 2452 TACGGTTTCA CGGGAGCGAGCA CGGACTCTGCGCTGCTGCAAGTGGCGGACGCTG 2511  
Qy 2521 ACGCAATCGGCGCGAGATGCTCTCGAGCGCGCTAGCTGCA CGCGGCTGGGG 2580  
Db 2512 ACGCAATCGGCGCGAGATGCTCTCGAGCGCGCGGATCGCGGCGCCCGGCTCG 2571  
Qy 2581 GAGTTGATCAGCTGCTGGCGCATTTTCGGAGGGCGCGGATCGCGGCGCCCGGCTCG 2640  
Db 2572 GCCTTCGAACAGCTCTGCGCGCATTTTCGGAGGGCGCGCATCGCGGCGCCCGGCGC 2631  
Qy 2641 TACTCCATCGCATCATCTAGCGGACACGACTCCATTTTCTGTTTGTGCGCGGCTC 2700  
Db 2632 TATTCATCGCATCATCTAGCGGACACGACTCCATCTTTGTGCTGTGCGCGGCTC 2691  
Qy 2701 ACGGCGGGGCTGGTGGCCATGCGCGACAAAGATGGCGAGCCACATCTCGCGCGCTG 2760  
Db 2692 ACGGCGCGGGCTGACGCGCGTGGCGCAAGA TGGCGAGCCATCTCGCGCGGCTG 2751  
Qy 2761 TTCTCTCCCCGATCAAGCTCAGTGGCGAAAGGTTTCAAGGCTGCTGCTCATCGC 2820  
Db 2752 TTCTCTCCCCATCAAACTCAGTGGCGAAAGACGTTTCAAGGCTGCTGCTCATCGC 2811  
Qy 2821 AAGAAAAAGTACATCGGCTCATCTCGGGGCAAGATGCTCATCAAGGGCTGATCTG 2880  
Db 2812 AAGAAAAAGTACATCGGCTCATCTA CGGGGTAGATGCTCATCAAGGGCTGATCTG 2871  
Qy 2881 GTGCGCAAAAACTGCTGCGTTTATCAACCGCACCTCAAGGCGCTGCTGCTGCTG 2940  
Db 2872 GTGCGCAAAAACTGCGCGTTTATCAACCGCACCTCAAGGCGCTGCTGCTGCTGCTG 2931  
Qy 2941 TTTTACGAGATACCGTATCGGAGCGCGCGCGGTTAGCGAGCGCGCCCGCAGAGGAG 3000  
Db 2932 TTTTACGAGATACCGTATCGGAGCGCGCGCGGTTAGCGAGCGCGCCCGCAGAGGAG 2991  
Qy 3001 TGGCTGGCGGACCCCTGCGGAGGGA CTGAGGCGTTTCGGGCGCTCTCTGATAGCGC 3060  
Db 2992 TGGCTGGCGGACCCCTGCGGAGGGA CTGAGGCGTTTCGGGCGCTCTCTGATAGCGC 3051  
Qy 3061 CATCGCGGATCA CGGACCGGAGAGGACATCAAGGACTTTGTCTCTCA CGCGGAACTG 3120  
Db 3052 CATCGCGGATCA CGGACCGGAGAGGACATCAAGGACTTTGTCTCTCA CGCGGAACTG 3111  
Qy 3121 AGCAGACCCCGCGCGTACCAACAGCGCTTGGCCCACTGACGCTGTATTACAAG 3180  
Db 3112 AGCAGACCCCGCGCGTACCAACAGCGCTTGGCCCACTGACGCTGTATTACAAG 3171  
Qy 3181 CTCTGCGCGCGCGGCTCGCTCCATCAAGGACCGGATCCCCGTA CGTGTGCTG 3240  
Db 3172 CTCTGCGCGCGCGGCTCGCTCCATCAAGGACCGGATCCCCGTA CGTGTGCTG 3231  
Qy 3241 GCCCAGACCCCGGAGGTAGAGAGCGGTGCGGGCTGGCGGCTCTCGCGAGCTAGAC 3300  
Db 3232 GCCCAGACCCCGGAGGTAGAGAGCGGTGCGGGCTGGCGGCTCTCGCGAGCTAGAC 3291  
Qy 3301 GCCCGCGCGCGGAGGAGCGCCCGCCCGAGCGGCTGCTCTCCCGGCGAGCGC 3360  
Db 3292 GCCCGCGCGCGGAGGAGCGCCCGCCCGCGGCGCTGCTCTCCCGGCGAGCGC 3351  
Qy 3361 CCCCGGAGAGCGCGCTGCTGCGACCCCGCGGAGGCGCTCAAGCGCCCGGAGCTG 3420  
Db 3352 CCCCGGAGAGCGCGCTGCTGCGACCCCGCGGAGGCGCTCAAGCGCCCGGAGCTG 3411



QY 3421 CTGGTGTCCGAGCTGGCGGAGGATCCCGGTACGCCATCCCGCGGCGCTTCGGCTCAAC 3480  
Db |||||  
QY 3412 CTGGTGTCCGAGCTGGCGGAGGATCCCGCATCGCCATGCCCCACGCGCTGCGCCCTGAAC 3471  
Db |||||  
QY 3481 ACGGACTATTACTTCTCGGACCTGTCTGGGGCGGCGCTGCGTGACGTTTCAAGGCCCTGTGTT 3540  
Db |||||  
QY 3472 ACGGACTATTACTTCTCCACCTGTGTTGGGGCGGCGTGCCTGACATTTCAAGGCCCTGTGTT 3531  
QY 3541 GGAAATAAGCCCAAGATCACCGAGAGTCTGTTAAAGAGGTTTATTTCCCGAGAGCTGCGCAC 3600  
Db |||||  
QY 3532 GGGAAATAACCCCAAGATCACCGAGAGTCTGTTAAAGGTTTATTTCCCGAAGTGTGGCAC 3591  
QY 3601 CCCCGGAGACGCTGGCGCGCGGCTCAGGGCCGCGGGTTCGGGCGGCGGGGCGGCG 3660  
Db |||||  
QY 3592 CCCCCGAGACGCTGGCGCGGCTCCGGCCGCGAGGTTCCGGGGCGTGGGTGCGGCG 3651  
QY 3661 GCTACGGCGAGGAAACTCGTCAATGTTGCTAGAGAGCTTTGATATCTCTAGCATGA 3717  
Db |||||  
QY 3652 GCTACGGCGGAGGAAACTCGTCAATGTTGCTAGAGAGCTTTGATATCTCTAGCATGA 3708

## RESULT 7

US-09-904-065-9  
; Sequence 9, Application US/09904065  
; Patent No. 6682892  
; GENERAL INFORMATION:  
; APPLICANT: Homa, Fred  
; APPLICANT: Wathen, Michael  
; APPLICANT: Hopkins, Todd  
; APPLICANT: Thomsen, Darrell  
; TITLE OF INVENTION: A Method for Treating Herpes Virus  
; FILE REFERENCE: 00221  
; CURRENT APPLICATION NUMBER: US/09/904,065  
; CURRENT FILING DATE: 2001-07-12  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 3708  
; TYPE: DNA  
; ORGANISM: herpes simplex  
US-09-904-065-9

Query Match 82.0%; Score 3047; DB 4; Length 3708;  
Best Local Similarity 89.1%; Pred. No. 0;  
Matches 3313; Conservative 0; Mismatches 395; Indels 9; Gaps 2;

QY 1 ATGTTTGTGCGCGGCGGCGCCGACTTCCCGGGGGGAAAGTTCGGCGGCTCGGGCGG 60  
Db |||||  
QY 1 ATGTTTGTGCGGCGGCGGCGCTGTCCCGGAGGAAAGTTCGGCGGCGGCGGCGG 60  
QY 61 TCTGGGTGTTTTCGCCCCCAACCCCGGGGAGCCACCAGACGGCACCGCGCTTCG 120  
Db |||||  
QY 61 TCGGGGTGTTTTCGGCGCGCGGCGCTTCGGGAGCGCGCC---GGGAGCCCCCGCTGT 117  
QY 121 CGCGCGCAGAACTTCTACAAACCCCACTCGCTCAGACCGGAAAGCAGCAGGAGCGCC 180  
Db |||||  
QY 118 TTGAGGCAAACTTTTACAAACCCCTACTTCGCCCTCGGAGCGCAACAGAGCCGACC 177  
QY 181 GGGCGGGCTCAGCGCATAGTACTACAGGAGTGCAGCAATTTTCGATTTATCGCCCCG 240  
Db |||||  
QY 178 GGGCCAAACCCAGCGCCATAGTACTATAGCAATGCGATGAATTTTCGATTCGCGCCG 237  
QY 241 CGTTTCCTGGACGAGGAGCCCGCGGAGCGACCGCGGGTTCACGACGCGCCCTC 300  
Db |||||  
QY 238 CGGGTCTGGACGAGGATGCCCCCGGAGAGCGCGCGGGTGCACGACGCTCACCTC 297  
QY 301 CGCGCGCCCTTAAGGTGTACTCGGGGGGAGCAGCGGACGCTCTCCGCGTGGGCGCG 360  
Db |||||  
QY 298 AAGCGCGCCCAAGGTGTACTCGGGGGGAGCAGCGGACGCTCTCCGCGTGGGTGCG 357  
QY 361 GAGGGCTTCTGGCGCGCTCGCTTGGCCCTGTGGGCGGTGCGGACCATGCCCCCAAGGG 420  
Db |||||

Db 358 GGCGGCTTCTGGCGCGCGGCTCGCGCCTGTGGGGCGGCTGGAACACACCCCGCGGGG 417  
QY 421 TTTCGACCCACCGTCAACCGTCTTCCACGTGTAGACATCTCGAGACACGCTGGAAACGCG 480  
Db |||||  
QY 418 TTCAACCCACCGTCAACCGTCTTTCACGTGTATGACATCTTGAGAACTGAGACGCG 477  
QY 481 TACAGCATCGCGCGCGCCAGCTCCAAGAGGATTTATGAGACGCAATTCAGCGCCGCGG 540  
Db |||||  
QY 478 TAGGGCATCGCGCGCGCCAGTTCCACGCGCGGTTTATGAGCGCATCACACGCGGG 537  
QY 541 ACGTCATCAGCGTCTGGGTCTGACCCCGAAGGCATCGCGTCCGCGCTTCACTGCTAC 600  
Db |||||  
QY 538 ACCGTATCAGCGTCTGGGCTGACTCCGGAAGGCACCGGTGGCGCTTCACTGCTTAC 597  
QY 601 GGCAGCGCGAGTACTTTTACATGAACAAGGGGAGGTGATCGGCACTTCGCAAGTCCGT 660  
Db |||||  
QY 598 GGCAGCGCGAGTACTTTTACATGAACAAGGAGAGGTTGACAGGCACTTACATGCGCG 657  
QY 661 GCCCGCGCATCTCTGCGAGCGCTTGGCGGCGGCGCTTGGCGAGTCCGCGGGGCGTGC 720  
Db |||||  
QY 658 GCCCCACGAGATCTCTGCGAGCGCATGGCCGCGGCGCTTGGCGAGTCCCGCGCGCTG 717  
QY 721 TTTCGGCGCATCTCGCGGACCATCTTCGAGGCGGAGGTGGTGGAGCGCGCGAGTGTAC 780  
Db |||||  
QY 718 TTTCGGCGCATCTCGCGGACCATCTTCGAGGCGGAGGTGGTGGAGCGCAACCGAGTGTAC 777  
QY 781 TATTAGGAACGCGCGCGGCTGTACTACCGCTCTTCGTCGAAGCGGCGCGCGCTG 840  
Db |||||  
QY 778 TACTAGGAGCGCGCGCGCTCTGTGTTTACCGGCTCTAGTCCGAAGCGGCGCGCTG 837  
QY 841 GCTACTCTGCGCAAACTTTTGGCCCGGATCAGGAAGTACAGAGGGGCGTTCGACGCC 900  
Db |||||  
QY 838 TCGTACTCTGCGCAAACTTCTGCCCGGCATCAAGAAGTACGAGGCTGGGTCGACGCC 897  
QY 901 ACCACCGGTTTATCTCGACAAACCGGGGTTTGTCACTTGGCTGGTACCGCTCAAG 960  
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QY 898 ACCACCGGTTTATCTCGTGAACAAACCGGGTTCGTCACTTGGCTGGTACCGCTCAAA 957  
QY 961 CCGCGCGGGGAAACGCGCGCGCCCAACCGCGCCCCCGACGCGCTTCGGAACCTCGAGC 1020  
Db |||||  
QY 958 CCGGGCGGAAACAAACGCTAGCCAGCCCGGGCCCCGATGGCCTTCGGGACATCAGC 1017  
QY 1021 GAGCTGAGTTTAACTGCAAGCGGCAACCTTGGCGCTCGAGGGGCGCATGTGTGACCTG 1080  
Db |||||  
QY 1018 GATGTCGAGTTTAACTGTACGCGGACAACTTGGCCATCGAGGGGCGCATGACGACCTA 1077  
QY 1081 CCGGCTTACAGCTCATGTCTTCGATTCGAATGCAAGCGCGGGGGAGGAGCAGAGCTG 1140  
Db |||||  
QY 1078 CCGGCATACAGCTCATGTGTTTCGATATCGAATGCAAGCGCGGGGGGAGGAGCAGCTG 1137  
QY 1141 GCCTTTTCGGTTCGGAACGCGCGGAAAGACTTCGTATCCAGATCTCTGTCTGCTCTAC 1200  
Db |||||  
QY 1138 GCCTTTCGGTTCGGGACCCCGGAGGACTTGTGTATCCAGATATCTGTCTGCTCTAC 1197  
QY 1201 GACCTGTCCACCAACCGCTTCGAGCAGATCTCTCTGTTTTCGTTCGGATCTCTGCACTC 1260  
Db |||||  
QY 1198 GACCTGTCCACCAACCGCTTCGAGCAGCTCTCTCTGTTTTCGTTCGGTTCCTGCGACCTC 1257  
QY 1261 CCGGAGTCCCACTCAGCGATCTCGCTCCAGGGGCTCGCGGCCCCCGCTGCTCTGGAG 1320  
Db |||||  
QY 1258 CCGGAATCCCACTGAACGAGCTGGCGGCTGCGGCGCTGCCCAACCGCGCTGTTCTGGA 1317  
QY 1321 TTTGACAGGAATTCGAGATGCTGTGGCTTTCATGACCTTCGTCAAGCAGTACGCGCCC 1380  
Db |||||  
QY 1318 TTTCGACAGGAATTCGAGATGCTGTGGCTTTCATGACCTTGTGAAACATGACGCGCCC 1377  
QY 1381 GAGTTCGTGACCGGGTACAACTCATCAACTTCGATGCGCCCTTCGTCTGACCAAGCTG 1440  
Db |||||  
QY 1378 GAGTTCGTGACCGGGTACAACTCATCAACTTCGATGCGCCCTTCTTCTGCGCAAGCTG 1437  
QY 1441 ACGGAGATCTCAAGGTCCCGCTCGACGGGTACGGGCGCATGAAACCGCGGGGTGTGTTTC 1500  
Db |||||  
QY 1438 ACGGAGATTTTCAAGGTCCCGCTTGGACGGGTACGGCGCATGAAACCGCGGGCGTGTGTTT 1497





; LENGTH: 1654			
5223391-4			
Query Match			
Best Local Similarity 30.0%; Score 1116.6; DB 6; Length 1654;			
Matches 1373; Conservative 0; Mismatches 184; Indels 106; Gaps 4;			
QY	1351	TTTCATGACCTTCTGTCAGACAGTACGGCCCGCGAGTTCTGTGACCGGTACAACTATCAAC	1410
DB	1	TTTCATGACCTTGTGAACACAGTACGGCCCGCGAGTTCTGTGACCGGTACAACTATCAAC	60
QY	1411	TTTCGACTGCGCTTCTGTCGACCAAGCTGACGGAGATCTACAAG-GTCCGCTCGAGG	1469
DB	61	TTTCGACTGCGCTTCTGTCGCGCAAGCTGACGGACATTTACAAGTTGTCCTCGACCG	120
QY	1470	GTACGGGCGCATGAACGGCGGGGTGTGTTCCGCGTGTGGGACATCGGCGAGAGCCACTT	1529
DB	121	GTACGGCGCATGAACGGCGGGCGGTGTTTCGCGTGTGGGACATAGGCCAGAGCCACTT	180
QY	1530	TCAGAAAGCCGACAGATCAAGGTGAACGGGATGTTGAACATCGACATGTACGGATCAT	1589
DB	181	CCAGAAAGCGCAGCAAGATGAAGGTGAACGGGCATGTGTGAACATCGACATGTACGGATCAT	240
QY	1590	CACCGACAAAGTCAAACTCTCAGCTTACAAGCTGAAGCGCGTGCAGGCGCGTCTTGAA	1649
DB	241	AACCGACAAGATCAAGCTCTCAGCTACAGCTCAAGCTCAAGCGCTGCGGAAGCCGTCGAA	300
QY	1650	GGACAAGAAAGGATCTGAGCTACCGGACATCCCGCCTACTACGCTCCGGGCGCGC	1709
DB	301	GGACAAGAAAGGACCTGAGCTATCGGACATCCCGCCTACTACGCCACCGGGCGCGC	360
QY	1710	GCAGCGGGGTGATCGGCGAGTATGTGTGAGGACTCGCTGCTGCTGGCGAGCTGTT	1769
DB	361	GCAACGCGGGGTGATCGGCGAGTACTGACATACAGATTCCCTGCTGGTGGCGCAGCTGTT	420
QY	1770	CTTCAAGTTTCTCGCGCACTCGAGCTTTCGCGCGTTCGCGCGCTCGCGCGGATCAACAT	1829
DB	421	TTTTTAAGTTTTCGCCCATCTCGAGCTCTCGCGCTTCGCGCGCTGGCGGTATTAACT	480
QY	1830	CACCGCACCATCTACGAGCGGACAGATCCGCGTCTTCAGTGCCTCTCGCGCTTGC	1889
DB	481	CACCGCACCATCTACGAGCGGACAGATCCGCGTCTTCAGTGCCTCTCGCGCTTGC	540
QY	1890	GGGCGAGAGGCTTCATCTCCCGGACACCCAGGGCGGTTTCGGGCGCTCGACAGGA	1949
DB	541	CGACAGAAAGGCTTATTTCTGCGGACACCCAGGGCGGATTAGGGGCGCGCGGGGGA	600
QY	1950	GGCGCCCAAGCGCGCGCGTCTCGGGGGAAGGGGAGCGCGCGGGGAGCGGAAACGG	2009
DB	601	GGCGCCCAAGCGTCCGGCCCGAGCCCGGAGACGAGGAGCGGCCAGAGG-----AGGA	654
QY	2010	GGACGAGATTAAGACGACGACGAGAGGAGGAGCGGGGACGAGCGGAGAGGTCCGCGG	2069
DB	655	GGGGGAGGACGAGGACGACGAGGAGGCGGGGCGAGCGGAGCGGAGCGGGCGCGG	714
QY	2070	CGAGACCGGGGCGCGCGCTTTGGGTACGAGGGGCGCGGGTCTCGACCCACCTCCGG	2129
DB	715	GGAGACCGCGCGCGCGCTTTGGGTACGAGGGGCGAACGCTCTTGACCCCACTTCGG	774
QY	2130	GTTCACGTCGACCCCGTGGTGTGTTGACTTTCGACGCTGTATCCCGACGATCATCA	2189
DB	775	GTTCACGTCGACCCCGTGGTGTGTTGACTTTCGACGCTGTATCCCGACGATCATCA	831
QY	2190	GGCCCAACACTGTGTTTTCAGTACGCTCTCCCTCGCGGCGGAGCGGCTCGGACCTGGA	2249
DB	832	GGCCCAACACTGTGTTTTCAGTACGCTCTCCCTCGAGGCGGAGCGGAGCTGGA	891
QY	2250	GGCGACCGGACTACTCGAGATCGAGGTGGGGCGGAGCGGCTGTTCTTCGTAGAGC	2309
DB	892	GGCGGCAAGGACTACTCGAGATCGAGGTGGGGCGGAGCGGCTGTTCTTCGTAGAGC	951
QY	2310	CCACGTCAGCGAGGCTCTCGAGCATCTG-----GGGGAACCCCGCGCTTGT	2340
DB	952	TCAGTCGAGAGAGCCTCTCTCAGCATCTCTCTCGGGAGCTGGCTCGCATCGAAAGCA	1011
QY	2341	-----	2340
DB	1012	GATCGCTCGCGATTCCCGAGAGCAGCCCGAGGAGGCGGTGCGAGAGAGCTCTCTCAG	1071
QY	2341	-----CTGGCGGACTGGCTGGCCATCGGAAGCAGATCCGCTCGCGATCCCCAGAG	2393
DB	1072	CATCTCTCTGGGGACTGGCTCGCCATCGGAAGCAGATCCGCTCGCGATTTCCCGAG	1131
QY	2394	CACCCCGGAGAGGCGCTCTCTCGACAAGCAACAGGCGCGCATCAAGGTGGTGTGAA	2453
DB	1132	CAGCCCGAGAGGCGGTCTCTCTCGACAAGCAGCAGCGCGCCATCAAGTCTGTGTAA	1191
QY	2454	CTCGGTGTACGGGTTCACCGGGGCGCAGACGGTCTTCTGCGCTCTCTGACGTGGCGCG	2513
DB	1192	CTCGGTGTACGGGTTCACCGGGGCTGACGCGAGTGTCTGCGCTCTCTGACGTGGCGCG	1251
QY	2514	CACCGTGAAGACCATCGGCGCGAGATCTCTCTCGGACGCGCGGTAGCTGACGCGG	2573
DB	1252	GACGCTGACGACCATCGGCGCGAGATCTCTCTCGGACCGCGGAGTCACTCCAGCGG	1311
QY	2574	CTGGGCGGAGTTCGATCAGCTGCTGCGCGACTTTTCCGGAGGCGCGGATCGCGCGCC	2633
DB	1312	CTGGGCGGCTTCGAAAGCTCTCTGCGCGATTTCGCGAGGCGCGGACATCGCGCGCC	1371
QY	2634	CGGTCCGTATCTCATGCGCATCATCTACGGGAGACAGGACTCCATTTTGTGTCGG	2693
DB	1372	CGGGCCCTATTTCATGCGCATCATCTACGGGAGACAGGACTCCATTTTGTGTCGG	1431
QY	2694	CGGCTCTACGGCGCGGCGCTGTGCGCATGCGGACCAAGATGGGAGCCACATCTCGG	2753
DB	1432	CGGCTCTACGGCGCGGCGCTGTGCGCATGCGGACCAAGATGGGAGCCACATCTCGG	1491
QY	2754	CGCGTGTCTCTCCCGCGATCAAGCTCGAGTGCAGAAAAGCTTCAACAAGCTCTGCT	2813
DB	1492	CGCGTGTCTCTCCCGCGATCAAGCTCGAGTGCAGAAAAGCTTCAACAAGCTCTGCT	1551
QY	2814	CATCCCAAGAAAAGTACATCGGCTCATCTCGGGGCGGAGATGCTCATCAAGGGGT	2873
DB	1552	GATCCCAAGAAAAGTACATCGGCTCATCTCGGGGCGGAGATGCTCATCAAGGGGT	1611
QY	2874	GSATCTGTGCGCAAAAACACTGCGCTTTTATCAACCGCAC	2916
DB	1612	GSATCTGTGCGCAAAAACACTGCGCTTTTATCAACCGCAC	1654
RESULT 10			
5223391-1			
; Patent No. 5223391			
; APPLICANT: COEN, DONALD M.; DIGARD, PAUL E.			
; TITLE OF INVENTION: INHIBITORS OF HERPES SIMPLEX VIRUS			
; REPLICATION			
; NUMBER OF SEQUENCES: 9			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/07/482,634			
; FILING DATE: 21-FEB-1990			
; SEQ ID NO:1:			
; LENGTH: 1678			
5223391-1			
Query Match			
Best Local Similarity 27.1%; Score 1005.8; DB 6; Length 1678;			
Matches 1148; Conservative 0; Mismatches 197; Indels 4; Gaps 2;			
QY	3	GTGTTGTGCGCGGGCGCGCGACTTCCCGCGGGGGAAGTCGGGGCTCGGGCGCGCTC	62
DB	333	GATGTTTTTCGGTGGCGCGCGCTGTCCTCCCGGAGAAAAGTCGGCGGCCGAGGCGCGCTC	392
QY	63	TGGGTTTTTGGCCCCCAACACCCCGGGGAGCCACCCAGAGCGGACCGCGCGCTTGGCG	122
DB	393	CGGGTTTTTGGCGCGCGCGCGCTCTCGCGGAGCGCGCC---GGGGAACCCCGCGCTTGT	449

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QY 123 CCGCGAGAACTTCTACAAACCCCACTCGCTCAGACCGGAACGAGCAAAAGGCCCGG 182
Db 123 CCGCGAGAACTTCTACAAACCCCACTCGCTCAGACCGGAACGAGCAAAAGGCCCGG 182
QY 450 GAGGCAAACTTTTACAAACCCCACTCGCTCAGACCGGAACGAGCAAAAGGCCCGG 509
Db 450 GAGGCAAACTTTTACAAACCCCACTCGCTCAGACCGGAACGAGCAAAAGGCCCGG 509
QY 183 GCGGGCTCAGGCGCATAGTACTACAGGAGTGGAGCAATTTTCGATTTATCGCCCGCG 242
Db 183 GCGGGCTCAGGCGCATAGTACTACAGGAGTGGAGCAATTTTCGATTTATCGCCCGCG 242
QY 510 GCCAACCCGCGCATAGTACTATAGCGAATTCGATTTTCGATTTATCGCCCGCG 569
Db 510 GCCAACCCGCGCATAGTACTATAGCGAATTCGATTTTCGATTTATCGCCCGCG 569
QY 243 TTGCTGGAGAGGAGCCCGCGGAGCAGCGCAACCGGGGTTCACGACGCGCGCTCCG 302
Db 243 TTGCTGGAGAGGAGCCCGCGGAGCAGCGCAACCGGGGTTCACGACGCGCGCTCCG 302
QY 570 GGTGCTGGAGAGGAGCCCGCGGAGCAGCGCAACCGGGGTTCACGACGCGCTCCG 629
Db 570 GGTGCTGGAGAGGAGCCCGCGGAGCAGCGCAACCGGGGTTCACGACGCGCTCCG 629
QY 303 GCGGCGCCCTTAAGTGTACTCTGCGGGGGGAGCGAGCGGAGCTCTCGGTCGGCGCG 362
Db 303 GCGGCGCCCTTAAGTGTACTCTGCGGGGGGAGCGAGCGGAGCTCTCGGTCGGCGCG 362
QY 630 GCGGCGCCCTTAAGTGTACTCTGCGGGGGGAGCGAGCGGAGCTCTCGGTCGGCGCG 689
Db 630 GCGGCGCCCTTAAGTGTACTCTGCGGGGGGAGCGAGCGGAGCTCTCGGTCGGCGCG 689
QY 363 GCGGCTTCTGCGCGCTCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 422
Db 363 GCGGCTTCTGCGCGCTCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 422
QY 690 CCGGCTTCTGCGCGCTCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 749
Db 690 CCGGCTTCTGCGCGCTCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 749
QY 423 CGACCCCAACGCTTCTGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 482
Db 423 CGACCCCAACGCTTCTGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 482
QY 750 CAACCCCAACGCTTCTGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 809
Db 750 CAACCCCAACGCTTCTGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 809
QY 483 CAGCATGCGCGCGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 542
Db 483 CAGCATGCGCGCGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 542
QY 810 CCGCATGCGCGCGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 869
Db 810 CCGCATGCGCGCGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 869
QY 543 CGTCATCAGCGCTTCTGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 602
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Db 930 CACGCGGAGTACTTTTACATGAACAAAGCGAGGTGGATCGCACCTCAGTTCGCTGC 989
QY 663 CCGCGCGAGTCTCTGCGAGCGCTTGGCGCGCGCTTGGCGCGCGCTTGGCGCGCGCT 722
Db 663 CCGCGCGAGTCTCTGCGAGCGCTTGGCGCGCGCTTGGCGCGCGCTTGGCGCGCGCT 722
QY 990 CCGCGAGATCTCTGCGAGCGCTTGGCGCGCGCTTGGCGCGCGCTTGGCGCGCGCT 1049
Db 990 CCGCGAGATCTCTGCGAGCGCTTGGCGCGCGCTTGGCGCGCGCTTGGCGCGCGCT 1049
QY 723 CCGGCGCATCTCGCGGAGCACTTGGAGGCGAGGTGGAGCGCGCGCGCTTGGAGCTA 782
Db 723 CCGGCGCATCTCGCGGAGCACTTGGAGGCGAGGTGGAGCGCGCGCGCTTGGAGCTA 782
QY 1050 CCGCGGAGTCTCGCGGAGCACTTGGAGGCGAGGTGGAGCGCGCGCGCTTGGAGCTA 1109
Db 1050 CCGCGGAGTCTCGCGGAGCACTTGGAGGCGAGGTGGAGCGCGCGCGCTTGGAGCTA 1109
QY 783 TTACGAAACCGCGCGCGCTTACTACCGCTTCTGCGGAGCGGCGCGCGCTTGGC 842
Db 783 TTACGAAACCGCGCGCGCTTACTACCGCTTCTGCGGAGCGGCGCGCGCTTGGC 842
QY 1110 CTACGAGACCGCGCGCGCTTCTGTTTACCGCTTCTGCGGAGCGGCGCGCTTGGC 1169
Db 1110 CTACGAGACCGCGCGCGCTTCTGTTTACCGCTTCTGCGGAGCGGCGCGCTTGGC 1169
QY 843 CTACCTGTGCGAACAATTTTCCCGCGATCAGGAAATCAGAGGGGGCGCTCGACGCCAC 902
Db 843 CTACCTGTGCGAACAATTTTCCCGCGATCAGGAAATCAGAGGGGGCGCTCGACGCCAC 902
QY 1170 GTACCTGTGCGAACAATTTTCCCGCGATCAGGAAATCAGAGGGGGCGCTCGACGCCAC 1229
Db 1170 GTACCTGTGCGAACAATTTTCCCGCGATCAGGAAATCAGAGGGGGCGCTCGACGCCAC 1229
QY 903 CACCGGTTTATCTGAGAACCGCGGGTTTGTACCTTGGCTTGGTAACGCTTCAAGCC 962
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QY 1230 CACCGGTTTATCTGAGAACCGCGGGTTTGTACCTTGGCTTGGTAACGCTTCAAGCC 1289
Db 1230 CACCGGTTTATCTGAGAACCGCGGGTTTGTACCTTGGCTTGGTAACGCTTCAAGCC 1289
QY 963 CCGCGCGGAAACGCGCGCGCGCAACCGCGCGCGCGCGCGCGCGCTTGGAGCTCAGCG 1022
Db 963 CCGCGCGGAAACGCGCGCGCGCAACCGCGCGCGCGCGCGCGCGCTTGGAGCTCAGCG 1022
QY 1290 GCGCGGAAACGCGCGCGCGCAACCGCGCGCGCGCGCGCGCGCTTGGAGCTCAGCG 1349
Db 1290 GCGCGGAAACGCGCGCGCGCAACCGCGCGCGCGCGCGCGCGCTTGGAGCTCAGCG 1349
QY 1023 CGTCGAGTTTAACTGACGCGGAGCAACCTGCGCGCGCGCGCGCGCGCTTGGAGCTCAGCG 1082
Db 1023 CGTCGAGTTTAACTGACGCGGAGCAACCTGCGCGCGCGCGCGCGCGCTTGGAGCTCAGCG 1082
QY 1350 CGTGGAGTTTAACTGACGCGGAGCAACCTGCGCGCGCGCGCGCGCGCTTGGAGCTCAGCG 1409
Db 1350 CGTGGAGTTTAACTGACGCGGAGCAACCTGCGCGCGCGCGCGCGCGCTTGGAGCTCAGCG 1409
QY 1083 GCGCTACAGCTCATGTGCTTGCATTCGAATCGAAGGCGCGGGGGAGGAGCGAGCTGGC 1142
Db 1083 GCGCTACAGCTCATGTGCTTGCATTCGAATCGAAGGCGCGGGGGAGGAGCGAGCTGGC 1142
QY 1410 GGCATCAAGCTCATGTGCTTGCATTCGAATCGAAGGCGCGGGGGAGGAGCGAGCTGGC 1469
Db 1410 GGCATCAAGCTCATGTGCTTGCATTCGAATCGAAGGCGCGGGGGAGGAGCGAGCTGGC 1469
QY 1143 CTTTTCG-GTCGCGGAGCGCGCGGAGCTCGTCATCCAGATCTCTGCTCTCTAGC 1201
Db 1143 CTTTTCG-GTCGCGGAGCGCGCGGAGCTCGTCATCCAGATCTCTGCTCTCTAGC 1201
QY 1470 CTTTTCGCTGGCGCGGAGCGCGGAGCTCTGCTTATGATCATCTCTGCTCTAGC 1529
Db 1470 CTTTTCGCTGGCGCGGAGCGCGGAGCTCTGCTTATGATCATCTCTGCTCTAGC 1529
QY 1202 ACCTGTCCACACCGCGCTCGAGCACATCTCTCTGTTTTCGCTCGGATCTCTGCGACCTCC 1261
Db 1202 ACCTGTCCACACCGCGCTCGAGCACATCTCTCTGTTTTCGCTCGGATCTCTGCGACCTCC 1261
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Db 1530 ACCTGTCCACACCGCGCTCGAGCACATCTCTCTGTTTTCGCTCGGTTCTCGGACCTCC 1589
QY 1262 CCGAGTCCACCTCAGGATCTCGCTCCAGGGGCTCGCGGCGCTCGCTCGTCTCGAGT 1321
Db 1590 CCGAATCCGACCTGAAACGAGCTGGCGGCCAGGGGCTGGCCACGCGCGTGGTTCTGGAAT 1649
QY 1322 TTGACAGCGAATTCGAGATGCTCTGGCC 1350
Db 1650 TCGACAGCGAATTCGAGATGCTCTGGCC 1678

RESULT 11
5223391-1
; Patent No. 5223391
; APPLICANT: COEN, DONALD M.; DIGARD, PAUL E.
; TITLE OF INVENTION: INHIBITORS OF HERPES SIMPLEX VIRUS
; REPLICATION
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/482,634
; FILING DATE: 21-FEB-1990
; SEQ ID NO: 1:
; LENGTH: 1678
5223391-1

Query Match 27.1%; Score 1005.8; DB 6; Length 1678;
Best Local Similarity 85.1%; Pred. No. 5.2e-186;
Matches 1148; Conservative 0; Mismatches 197; Indels 4; Gaps 2;

QY 3 GTTTTGTGCGCGCGCGCGCTTCCCGCGGGGGAAGTCCGCGGCTCGGCGGCGTC 62
Db 333 GATGTTTTCGCGTGGCGCGCTGTCCTCCCGAGGAAAGTCCGCGGCGGCGTC 392
QY 63 TGGGTTTTTGGCCCCCAACACCCCGGGGAGCACCCAGACGCGCGCTTCGCG 122
Db 393 CCGGTTTTTGGCGCGCGCGCTCGCGAGCGCGCC--GGGGACCCCGCGCTTGT 449
QY 123 CCGGCGAAGACTTCTACAAACCCCGCTCAGACCGGAAACGACGCAAGGCCCGCG 182
Db 450 GAGGCAAACTTTTACAAACCTTACCTCGCCCGAGTCGGGACGCAACAGAACGCGCG 509
QY 183 GCGCGCTCAGCGCCATACGTACTACAGCGAGTTCGACGAATTTTCGATTTATCGCCCGCG 242
Db 510 GCCAACCCGCGCCATACGTACTATAGCGAATTCGATGAATTTTCGATTTATCGCCCGCG 569
QY 243 TTGCTGGAGAGGAGCGCGCGCGGAGCAGCGCAACGGGGTTCAGACGCGCGCTTCG 302
Db 570 GGTGCTGGAGAGCATGCGCGCGCGCGCGCGCGCGCGCGCGCTCACCTCAA 629
QY 303 GCGCGCGCTTAAGTGTACTCTGCGGGGGGAGCGAGCGGAGCTCTCGGTCGGCGCGCG 362
Db 630 GCGCGCGCTTAAGTGTACTCTGCGGGGGGAGCGAGCGGAGCTCTCGGTCGGGTCGG 689
QY 363 GCGCTTCTGCGCGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 422
Db 690 CCGCTTCTGCGCGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 749
QY 423 CGACCCCAACGCTTCTGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 482
Db 750 CAACCCCAACGCTTCTGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 809
QY 483 CAGCATGCGCGCGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 542
Db 810 CCGCATGCGCGCGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 869
QY 543 CGTCATCAGCGCTTCTGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 602
Db 870 CGTCATCAGCGCTTCTGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 929
QY 603 CACGCGGAGTACTTTTACATGAACAAAGCGAGGTGGATTCGCGACCTCAGTTCGCTGC 662
Db 930 CACGCGGAGTACTTTTACATGAACAAAGCGAGGTGGATTCGCGACCTCAGTTCGCTGC 989
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QY 663 CCGCGCGATCTCTGGAGCGCTGGCGCGGCCCTTGGCGAGTGGCGGGGGCGTCTGTT 722  
| | | | |  
Db 990 CCCACGAGATCTCTGGAGCGATGGCGCGGCCCTTGGCGAGTCCC CGGGGCGTCTGTT 1049  
| | | | |  
QY 723 CCGCGCATCTCCGGGACCACTTCGAGCGGAGTGGTGGAGCGCGCGAGCTGTACTA 782  
| | | | |  
Db 1050 CCGCGCATCTCCGGGACCACTTCGAGCGGAGTGGTGGAGCGCACCGAGCTGTACTA 1109  
| | | | |  
QY 783 TTACGAAACCGCCCGACCTGTACTACCGCGTCTTCTGTGCGAAGCGGGCGCGCTGGC 842  
| | | | |  
Db 1110 CTACGAGACGCCCGCCGCTCTGTCTTACCGCGTCTACGTCGGAAGCGGCGCGTGTCTG 1169  
| | | | |  
QY 843 CTACCTGTGCGAACAATTTCGCCCGCGATCAGGAAGTACGAGGGGGGGGTTCGAGCCAC 902  
| | | | |  
Db 1170 GTACCTGTGCGAACAATTTCGCCCGCGCATCAAGAAGTACGAGGGGTGGGGTTCGAGCGCCAC 1229  
| | | | |  
QY 903 CACCCGGTTTATCTTGGACAAACCGGGGTTTGTCACTTTCGCTGTGTACCGCTCAAGCC 962  
| | | | |  
Db 1230 CACCCGGTTTATCTTGGACAAACCGGGGTTTGTCACTTTCGCTGTGTACCGCTCAAGCC 1289  
| | | | |  
QY 963 CCGCGCGGGAACCGCGCGGCCCAACCGCGCCCGCGAGCGGTTTCGGAACCTTCGAGCGA 1022  
| | | | |  
Db 1290 GGGCCGGAACAACACGCTAGGCCAGCGCGGGCCCGATGGCTTCGGGACATCCAGCGA 1349  
| | | | |  
QY 1023 CGTCGAGTTTAACTGACGCGCGGACAACTTGGCCGCTCGAGGGGGCCATGTGTACCTGGC 1082  
| | | | |  
Db 1350 CGTGGAGTTTAACTGACGCGCGGACAACTTGGCCATCGAGGGGGGCATCAGCGACCTACC 1409  
| | | | |  
QY 1083 GGCTTACAGCTCATGTGCTTCGATATCGAATCGAAGCGCGGGGAGGAGAGTGGC 1142  
| | | | |  
Db 1410 GGCATACAGCTCATGTGCTTCGATATCGAATCGAAGCGGGGAGGAGAGTGGC 1469  
| | | | |  
QY 1143 CTTTCCG-CTCGCGGAACCGCCCGGAAGACCTCGTCATCCAGATCTCTGTCTGTCTAGC 1201  
| | | | |  
Db 1470 CTTTCCGCTGGCGGGCACCGGAGACCTGTGTTATTGACATATCTGTCTGTCTAGC 1529  
| | | | |  
QY 1202 ACTGTCCACACCGCCCTCGAGCACATCTCTGTTCGCTCGGATCTCGGACCTCC 1261  
| | | | |  
Db 1530 ACTGTCCACACCGCCCTCGAGCACATCTCTGTTCGCTCGGATCTCTCGACCTCC 1589  
| | | | |  
QY 1262 CCGAGTCCACCTCAGCATCTCGCTCCAGGGGCTCGCGGCCCGCGCTCGTGGAGT 1321  
| | | | |  
Db 1590 CCGAATCCAGCTGAACGAGCTGGCGGCAGGGGCTGCCACGCCCGTGGTCTTGGAT 1649  
| | | | |  
QY 1322 TTGACAGCAATTCGAGATGCTGTGGCC 1350  
| | | | |  
Db 1650 TCGACAGCAATTCGAGATGCTGTGGCC 1678  
| | | | |

## RESULT 12

5223391-6  
; Patent No. 5223391  
; APPLICANT: COEN, DONALD M.; DIGARD, PAUL E.  
; TITLE OF INVENTION: INHIBITORS OF HERPES SIMPLEX VIRUS  
; REPLICATION  
; NUMBER OF SEQUENCES: 9  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/482,634  
; FILING DATE: 21-FEB-1990  
; SEQ ID NO: 6:  
; LENGTH: 944  
5223391-6

Query Match 19.5%; Score 726.6; DB 6; Length 944;  
Best Local Similarity 95.9%; Pred. No. 6.8e-132;  
Matches 768; Conservative 0; Mismatches 29; Indels 4; Gaps 2;

QY 2917 TCCAGGGCCCTGGTGCACCTGTCTTTTACGAGATACCGTATCCGAGCGCGCGCG 2976  
| | | | |  
Db 1 TCCAGGGCCCTGGTGCACCTGTCTTTTACGAGATACCGTATCCGAGCGCGCGCG 60  
| | | | |  
QY 2977 TTAGCGGAGCGCCCGCAGAGAGTGGCTGGCGGACCCCTGCGCGAGGAGTGCAGGGCG 3036  
| | | | |

Db 61 TTAGCGGAGCGCCCGCAGAGAGTGGCTGGCGGACCCCTTGCCTCCGAGGGACTGCAGGGC 120  
| | | | |  
QY 3037 TTGCGGGCGCTCTCGTAGAGCCCATCGGCGCATCACGACCCCGAGAGGAGACATCCAG 3096  
| | | | |  
Db 121 TTGCGGGCGCTCTCGTAGAGCCCATCGGCGCATCACGACCCCGAGAGGAGACATCCAG 180  
| | | | |  
QY 3097 GACTTTGTCTCAACCGCGAACTGAGAGAGACACCGCGCGGTACACCAACGAGCGCTG 3156  
| | | | |  
Db 181 GACTTTGTCTCAACCGCGAACTGAGAGAGACACCGCGCGGTACACCAACGAGCGCTG 240  
| | | | |  
QY 3157 GCCACCTGAGCGTGTATTACAAGCTCATGGCCGCGCGCGAGTCCCGTCCATCAAG 3216  
| | | | |  
Db 241 GCCACCTGAGCGTGTATTACAAGCTCATGGCCGCGCGCGAGTCCCGTCCATCAAG 300  
| | | | |  
QY 3217 GACCGGATCCCGTACGTGATCGTGCCAGACCCCGAGAGTAGAGAGACGTCGCGGG 3276  
| | | | |  
Db 301 GACCGGATCCCGTACGTGATCGTGCCAGACCCCGAGCTAGAGAGAGACGTCGCGGG 360  
| | | | |  
QY 3277 CTGGCGCGCTCCGCGAGCTAGACCGCGCGCCCGAGGGAGAGCGCCCGCCCGCGCG 3336  
| | | | |  
Db 361 CTGGCGCGCTCCGCGAGCTAGACCGCGCGCCCGAGGGAGAGCGCCCGCCCGCGCG 420  
| | | | |  
QY 3337 GCCCTGCGCTCCCGGCCAAGCGCCCGGAGAGCGCGTGCATGCCGACCCCGCGGA 3396  
| | | | |  
Db 421 GCCCTGCGCTCCCGGCCAAGCGCCCGGAGAGCGCGTGCATGCCGAGTCCCGCGGA 480  
| | | | |  
QY 3397 GCGCGTCCAAAGCCCGCAAGCTGTGTGTCGAGTCTGGCGGAGAGTCCCGGGTACGCC 3456  
| | | | |  
Db 481 GCGCGTCCAAAGCCCGCAAGCTGTGTGTCGAGTCTGGCGGAGAGTCCCGGGTACGCC 539  
| | | | |  
QY 3457 ATCGCGCGGGGTTCGCTCAACGAGACTATTACTTCTGCGACCTGCTGGGGGGCGCC 3516  
| | | | |  
Db 540 ATTGCCACGCGGTCCGCTGAACACGAGCTATTACTTCTCCACCTGTTGGGGGGCGCG 599  
| | | | |  
QY 3517 TCGGTGAGCTTCAAGGCCCTGTTTGGAAATAACGCAAGATCACCGAGAGTCTGTTAAAG 3576  
| | | | |  
Db 600 TCGGTGAGCTTCAAGGCCCTGTTTGGGAATAACGCAAGATCACCGAGAGTCTGTTAAA 659  
| | | | |  
QY 3577 AGGTTTATTCGAGAGACGTGGCACCCCGGACAGAGTGGCGCGCGCTCAGGGCGCGG 3636  
| | | | |  
Db 660 AGGTTTATTCGAGAGTGGCACCCCGGACAGAGTGGCGCGCGCTCAGGGCGCGCA 719  
| | | | |  
QY 3637 GGGTTCGGCGCGGGGGCGCGCTAGCGGAGGAACTCGTCAATGTTGCATAGA 3696  
| | | | |  
Db 720 GGGTTCGGCGCGGGTGGGTGC---CGCTACGCGGAGGAACTCGTCAATGTTGCATAGA 776  
| | | | |  
QY 3697 GCCTTTGATACCTCTAGCATGA 3717  
| | | | |  
Db 777 GCCTTTGATACCTCTAGCATGA 797  
| | | | |

## RESULT 13

5223391-6  
; Patent No. 5223391  
; APPLICANT: COEN, DONALD M.; DIGARD, PAUL E.  
; TITLE OF INVENTION: INHIBITORS OF HERPES SIMPLEX VIRUS  
; REPLICATION  
; NUMBER OF SEQUENCES: 9  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/482,634  
; FILING DATE: 21-FEB-1990  
; SEQ ID NO: 6:  
; LENGTH: 944  
5223391-6

Query Match 19.5%; Score 726.6; DB 6; Length 944;  
Best Local Similarity 95.9%; Pred. No. 6.8e-132;  
Matches 768; Conservative 0; Mismatches 29; Indels 4; Gaps 2;

QY 2917 TCCAGGGCCCTGGTGCACCTGTCTTTTACGAGATACCGTATCCGAGCGCGCGCG 2976  
| | | | |  
Db 1 TCCAGGGCCCTGGTGCACCTGTCTTTTACGAGATACCGTATCCGAGCGCGCGCG 60  
| | | | |



Qy	2977	TTAGCGGAGCGCCCGCAGAGGAGTGGTGJCGCGA	CCCCCTGCCCGCAGGGA	CTGCAGGCG	3036	
Db	61	TTAGCCGAGGCGCCCGCAGAGGAGTGGTGCGCGAC	CCCTTGC	CCCGCAGGGA	CTGCAGGCG	120
Qy	3037	TTCCGGGCGGCTCTCGTAGAGCGCCATCGGGCG	CATCACCGAC	CCGCGAGAGGGA	CATCCAG	3096
Db	121	TTCCGGGCGGCTCTCGTAGAGCGCCATCGGGCG	CATCACCGAC	CCGCGAGAGGGA	CATCCAG	180
Qy	3097	GACTTTGTCTCTACCGCGGA	ACTGAGCAGACACCCGCGCGTACACAA	CAAGAGCGGCTG	3156	
Db	181	GACTTTGTCTCTACCGCGGA	ACTGAGCAGACACCCGCGCGTACACAA	CAGAGCGGCTG	240	
Qy	3157	GCCCACTGACGGTGTTATTAAAGCTCATGGC	CCCGCGCGCGTAGCGAGTACGAGGAGAGCG	TGCGCGG	3216	
Db	241	GCCCACTGACGGTGTTATTAAAGCTCATGGC	CCCGCGCGCGTAGCGAGTACGAGGAGAGCG	TGCGCGG	300	
Qy	3217	GACCGGATCCGTA	CGTGATCGTGCCCGCAGACCCGCGAGTACGAGGAGAGCG	TGCGCGG	3276	
Db	301	GACCGGATCCGTA	CGTGATCGTGCCCGCAGACCCGCGAGTACGAGGAGAGCG	TGCGCGG	360	
Qy	3277	CTGGCGCCCTCTCCGCGAGCTAGACGCGCG	CGCCCGCAGGGACGAGCGCCCGCCCGAGCG	3336		
Db	361	CTGGCGCCCTCTCCGCGAGCTAGACGCGCG	CGCCCGCAGGGACGAGCGCCCGCCCGAGCG	420		
Qy	3337	GCCCTGCCCTCTCCCGGCGAAAGCGCCCGCG	GAGACGCGCTGCATGCCGAC	CCCCCGGGA	3396	
Db	421	GCCCTGCCCTCTCCCGGCGAAAGCGCCCGCG	GAGACGCGCTGCATGCCGAC	CCCCCGGGA	480	
Qy	3397	GGCGCTCCAAGCCCGCAAGCTGCTGGTGTCG	GAGCTGGCGGAGGATCCCGGGTACGCC	3456		
Db	481	GGCGCTCCAAGCCCGCAAGCTGCTGGTGTCG	GAGCTGGCGGAGGATCCCGGGTACGCC	539		
Qy	3457	ATCGCCCGGGCGTTCCGCTCAACACGGA	CTATTACTTCTCGACCTGCTGGGGGCGGC	3516		
Db	540	ATTCGCCACAGCGCTCGCCCTGAACACGGA	CTATTACTTCTCCACCTGTTGGGGGCGGC	599		
Qy	3517	TGCGTGACGTTCAAGGCCCTGTTTGGNAATAA	CGCCAGATACCGAGAGTCTGTTAAG	3576		
Db	600	TGCGTGACATTC	CAAGGCCCTGTTTGGGAATTAACGCCAAGAT	CAACCGAGAGTCTGTTTAAA	659	
Qy	3577	AGGTTTATTC	CCGAGACGTGGCACCCCGCGACGATGGCCGCGGCTCAGGGGCGCG	3636		
Db	660	AGGTTTATTC	CCGAGAGTGGACACCCCGCGACGATGGCCGCGGCTCAGGGGCGCG	719		
Qy	3637	GGGTTCCGGGCGCGGGGGCGGCGCTAC	CGCGGAGGAACCTCGTGAATGTTGCATAGA	3696		
Db	720	GGGTTCCGGGCGCGTGGTG	CGTGCATAGGAGTGGCGGCGGCTCAGGAGGAACTCGTGAATGTTGCATAGA	776		
Qy	3697	GCCTTTGATACTTAGCATGA	3717			
Db	777	GCCTTTGATACTTAGCATGA	797			

## RESULT 14

RESOL 14  
US-081-680-326-28  
Sequence 28, Application US/08680326  
Patent No. 5925733  
GENERAL INFORMATION:  
APPLICANT: TIMOTHY M.  
APPLICANT: ROSE, BOSCH, MARNIX  
APPLICANT: STRAND, KURT  
APPLICANT: TODARO, GEORGE J.  
TITLE OF INVENTION: DNA POLYMERASE OF GAMMA HERPES VIRUSES  
TITLE OF INVENTION: ASSOCIATED WITH KAPOSI'S SARCOMA AND RETROPERITONEAL  
TITLE OF INVENTION: FIBROMATOSIS  
NUMBER OF SEQUENCES: 152  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 Page Mill Road  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA

QY	835	GCCTGGCCTACCTGTGGACAACTTTTGGCCCGGATCAGGAAGTACGAGGGGGCGTC	894	1915	GACACCCAGGGCGGTTCGGGGCTTCGACCAAGAGAGCGCCCAAGCGCCCGCGCTGCT	1974
Db	775	TTTACAAATATCTTTGTGATAACTTTTCACCGGAGTTGAAGATATGAAGTACGGGTA	834	1855	GATGGGGATACCCAGCTACTTTTGAATATAAGGATGTTATTC	1898
QY	895	GAGCGCACCCACCGGTATCTCGACAAACCGGGGTTTGTCACTTGGCTGTGACCGC	954	1975	CGGGGGAAAGGGAGCGGCGGGGAGCGGGAAACGGGGACGAGGATAAGACGACGACGAG	2034
Db	835	GAGCTACCACTCGTTTCTAATGATATCCCGGCTTTGTAGTTTGGTTGGTATCAA	894	1899	-----CGATGTCGGGGATGTTGAGGAA	1920
QY	955	CTCAAGCCCGCGCGGGGAAACGGCGGGCCCAACCGCGCCCCCGGACGGCGGTTCGGAACC	1014	2035	GACGAGACGGGGACGAGCGGAGGAGGTGCGGCGGAGACGGGGCGCGACCTTGGG	2094
Db	895	CTAAAACTCGAGTTGATGGGAAACGTGTTCGAGTTCCGACCGGCAAGTCGCCAAATTAACG	954	1921	GAGATGGATGAAGACGAGAGCGTTTTCCTCCACTGGTACGTCAAGTGGGCGGAAATGAGA	1980
QY	1015	TCGAGGAGCTCGAGTTTAACTGACGCGGACACCTGGCCGTGCGAGGGGCCATGTGT	1074	2095	TACAGGGGGCGCGGTCTCGACCCCACTCCGGGTTTCACGTCCAGCCCGCTGTGTGTG	2154
Db	955	TTAAGCGAGTTGAAATGACTGCAATGTCGGATAATCTGCAGGCTATACCAACGATGAC	1014	1981	TATAAGAGACGAGGTTTGTGACCTGATAGGGATTTATATCGATCCGGTGTGCTA	2040
QY	1075	GACCTGCCGCCCTACAAGCTCATGTCTCGACGCGACACCTGGCCGTGCGAGGGGCCATGTGT	1134	2155	TTTGACTTTGCCAGCCTGTACCCAGCATCATCAGGCCCAACACTGTGTCTTCAAGTACG	2214
Db	1015	TCATGGCCTGACTACAGTTGTATGTTTCGATATGATGTAATGTAATCAGGAGATCTAAT	1074	2041	TTGGATTTTGCAGTTTATATCCAAATATAATTCAGGCCCATAACTTATGTTTACCACG	2100
QY	1135	GAGCTGGCCTTTCCGCTCCGGAACCGCCGGAAGACCTCGTCAATCCAGATCTCTGTCTG	1194	2215	CTCTCCCTGCGGCGGAGCGCTCGGCACCTGGAGGCGGACCGGAGTACTCTGGAGATC	2274
Db	1075	GAGCTGGCGTTTCCGATCAACAATCTGGAGGATCTTGTAAATCCAAATTTCTGTCTA	1134	2101	CTAACGTTTAAATTTTGAGACGTTTAAACGTTTGAATCCATCC--GATTATGCCACCTTT	2157
QY	1195	CTCTAGGACCTGTCACACACCGCCCTCGAGCATCTCTCTGTCTTTCGTCGATCCTGTC	1254	2275	GAGGTGGGGGCGGACGCTGTTCTTCGTGAAGGCCACGTACGCGAGAGCTGTCTGAGC	2334
Db	1135	TTATATTCAATCCCTCGACAGTCTTTTGAACAACATTTTACTGTTTTCCTTGGCTCTGT	1194	2158	ACAGTTGGAGGAAACGTCCTTTTGTGGCTCTAACGTTTCGAGAAAGTCTGTGGGT	2217
QY	1255	GACCTCCCGGAGTCCACCTCAGCGATCTCGCTCCAGGGGCGTCGCGGCCCGCTGCTC	1314	2335	ATCCTGCTGCGCACTGGCTGGCCATCGAAAGCAGATCCGCTCGCGATCCCCCAGAGC	2394
Db	1195	GACTTACCAAAAGGTATGTAAGAATAATGAAGAGCGGGGTTTACCGGAGCCGACTGTG	1254	2218	GTTCCTTTTAAAGACTGCTTGGCTATGCGCAAGGCTATTAGAGCGCATACCCGGAAGT	2277
QY	1315	CTGAGTTTGAAGCGAATTCAGATGCTGCTGGCTTCATGACCTTCGTCAAGCAGTAC	1374	2395	ACCCCGGAGGAGCGCTCTCTCGACAAGCAACAGCGCGCATCAAGTGGTGTGCAAC	2454
Db	1255	CTGAGTTTGTATAGTAGTAATTCAGAGTATTAATGTCATTTATGACCTCTGTAACACAGTAC	1314	2278	TCCTCAGATGAAGCAGTGTATTAGACAAACAAAGCCCGGATAAAAGTAGTTTGTAT	2337
QY	1375	GGCCCGGAGTTCGTGACCGGTTACACATCATCACTTCGACTGGCCCTTCGTCGACC	1434	2455	TCGGTGTACGGGTTTCAACCGGCGCAGCACGCTCTTCGCGCTGCTGCACTGTGCGCGC	2514
Db	1315	GCTCCGAGTTTGCCACAGGTATTAACATTTGTAATTTTGTATGGCGGTTTATATGAG	1374	2338	TCCGTGTACGGTTTACTTGGAGTTGCGCAGGGATTTCTGCCATGTTTATACGTAGCGCC	2397
QY	1435	AAGCTGACGGAGATCTACAAGGTCCCGCTCGACGGGTACGGCGCATGAACGGCGGGGT	1494	2515	ACCGTGAAGCAATCGCGCCGCGAGATGCTCTCGCAGACGCGCGCTACGTGACCGCGCG	2574
Db	1375	AACTTAATTTATATACAGTCTCAAGCTTGATGTTATGGCAGTATAAACCGTGGGGT	1434	2398	ACTGTCTACAAATTGGCCGTCAAATGTTATTAAGTACCAGAGATTATATCATATAAC	2457
QY	1495	GTGTTCCGCGTGTGGACATCGGCGCAGAGCCATTTTCAGAACGCGAGCAAGATCAAGTGT	1554	2575	TGGCGGAGTTTCCATCAGCTGCTGCGACATTTCCGGA--GGCGCGCGGATGCGCGC	2631
Db	1435	CTGTTTAAGATATGGATGTTGGCAATCCGGATTTACGCGACGAAGCAAGGTAAAGATC	1494	2458	TGGCGCGATTGAACGTTTATTAACAGCGTTTCCAGACATTTGAAGTAGCGTTCTCTCC	2517
QY	1555	AACGGATGGTGAACATCGACATGTACGCGCATCATCCCGACAAGGTCAAACTCTCCAGC	1614	2632	CCCGTCCGTACTCCATCGCATCATCTACGGGGACAGGACTCCATTTTCGTTTGTGTC	2691
Db	1495	AACGGTCTCATATCTCTGGATATGTATGCAATTTGCAACTGAAAAATTTAAACTCTCGAGT	1554	2518	CAAAAGCGTACGAGGTAAGGTTATATATGAGATACGGATTCTGTGTTATCCGATTC	2577
QY	1615	TACAGCTGAACCGCTCGCGAGGCGCTTTGAGGACAAAGAGGATCTGAGCTAC	1674	2692	CGCGCTCAACGCGCGCGGCTGGTGGCCATGCGGCGCAAGATGGCGAGCCACATCTCG	2751
Db	1555	TATAAATTAGATTGCTTGCAGTGAAGTCTAATAGTCCAGAGAGATTTCCTTAC	1614	2578	AAGGCTGTAGTTGTGAGGGGATAGTAAATTCGGCGAGAAAAATGGCACATATAATTTCA	2637
QY	1675	CGCGCATCCCGCTTACTACGCTCCGGGCCCGCGAGCGGGGTGATCGCGAGTAT	1734	2752	CGCGCTGTTCCTCCCGCATCAAGCTCAGTCCGAGGCGAAAAACCTTCAACAGCTGCTG	2811
Db	1615	AAAGACATTTCCGGATATTACGCTAGTGACCGAATACACGAGGAATTTATGGTGAATAT	1674	2638	ACGGCTGTGTTTGTCTCTTATAAAGTTGGAGTGTGAAAAAATTTTATAAAAACTTTTG	2697
QY	1735	TGTGTCAGACTCGCTGTGTCGGGAGCTGTTCTTCAAGTTTTCGCGCACCTTGGG	1794	2812	CTCATCGCAAGAAAAAGTACATCGGCTCATCTCGGGGGCAAGATGCTCATCAAGGCG	2871
Db	1675	TGTATACAGACTCGGCTCTTGGGGAAACTGTTTTTTTAAATATTTTACACACCTTGAG	1734	2698	CTTATAAACAAGAAAAAGTACATTTGGGTTAATTTACGCGGNAAGGTTTATGAAGGA	2757
QY	1795	CTTTCGCGCTCGCGGCTGGCGGCGATCAACATCACCCGCAACCATCTACGACGCCAG	1854	2872	GTGATCTGTGTGCGCAAAAAACAATCTGCGGTTTTATCAAACGCACTCCAGGGCCCTGTGTC	2931
Db	1735	TTATCGCGGTTGCAAGGCTAGCTAGAAATTAATTTAACCAAGGCTATTTACGAGGACAG	1794	2758	GTGCTGCTGTTTGAAGAAAAAAACAACCTGTCAAATTTTATAACGATTATGCGCGCAAACTGTA	2817
QY	1855	CAGATCCGCTTTCAGTGCCTCTCGCGCTTGGCGGCGCAAGAGGCTTCATCTCGCG	1914	2932	GACCTGCTGTTTTCAGCATACCTGATCCGAGCGCGCGCGCTTAGCCGAGCGCCCC	2991
Db	1795	CAGGTTAGGATTTACACCTGTTTATTAGGACTGGCTTCGTCGAGGAGTTCGAGGCGCTCTC	1854	2818	GAACTGTGTTTATATGACGACACCGCTCTCGCGTGTCTGCGCGGAGGCGGTGTGTGTTCC	2877
				2992	GCAGAGGAGTGGCTGGCGCGACCCCTGCGCGAGGAGTTCGAGGCGTTTCGGGGCGCTCTC	3051

Db 2878 ATTGCTGAATGAATAGACGGGCATGCCGTCTGGGATGGCCGGTTTGGACGATAAAT 2937  
Qy 3052 GTAGAGCCCATCGCGCATACCGACCCGGAGGAGGAGATCCAGGACTTTGTCCTACC 3111  
Db 2938 GCAGATGCATCGCAGATTAATACCCCAAAATGGATTAATAAGTTTGTATGAGC 2997  
Qy 3112 GCCGAATCTAGCAGACACCCGCGGTACACCAAAAGCGCTGGCCACCTGACGGTG 3171  
Db 2998 GCCGAGTTAGTGTCCACCATCCGCTACATAAACCGTGGCTCACTTAAAGTA 3057  
Qy 3172 TATTACAGCTCATGGCCCGCGCGAGGTCCGTCATCAAGACCGGATCCCGTAC 3231  
Db 3058 TATTATAAATTAGTAATGACAGAGGTCAATCCCAACGTTTCGAGAAAGCATCCCTTAT 3117  
Qy 3232 GTGATCGTGGCCAGACCCCGGAGGTAGAGG 3262  
Db 3118 GTTATTGTGGCCCCACAGAGGAAGTGGAGG 3148

RESULT 15  
US-09-661-596A-76/c  
; Sequence 76, Application US/09661596A  
; Patent No. 6528066  
; GENERAL INFORMATION:  
; APPLICANT: Santos, Richard  
; TITLE OF INVENTION: VARIANT VARICELLA-ZOSTER VIRUSES AND METHODS OF USE  
; FILE REFERENCE: 140.0011 0101  
; CURRENT APPLICATION NUMBER: US/09/661,596A  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: US 60/153,779  
; PRIOR FILING DATE: 1999-09-14  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 76  
; LENGTH: 124884  
; TYPE: DNA  
; ORGANISM: Varicella zoster  
US-09-661-596A-76

Query Match 18.9%; Score 701.8; DB 4; Length 124884;  
Best Local Similarity 53.7%; Pred. No. 1.1e-126;  
Matches 1659; Conservative 0; Mismatches 1312; Indels 120; Gaps 5;

Qy 223 TTTTCGATTTATCGCCCGGGTTCGCTGGAGGAGCGCCCGCGGAGCAGCGCACCGG 282  
Db 50510 TTTCAATTTTGGCCCTTAAATGTTTATGATGAAGATGTGCCCATGGAGAACGAAAGGG 50451  
Qy 283 GTCCAGCGCGCGCTCGCGCGCGCCCTAAGGTGTACTGGGGGGGACGAGCGGAC 342  
Db 50450 GTTCAGTGGTACACTTAGTCGACCGCTTAAAGTTTACTGTAATGGAAGAGTTCCG 50391  
Qy 343 GTCTCCGCGTGGCCCGGAGGGCTTCTGGCCGCGTGGTGGCGCTGGGGCGGTGGC 402  
Db 50390 ATTCTGGATTTTGTGTTTCCAGCCCTGGCCCTAGACGCGTGAATATTTGGGGGAAATC 50331  
Qy 403 GACCATGCCCCNAGGGTTCGACCCACCGTCACCGTCTTCCAGTGTACGACATCCTG 462  
Db 50330 GACTTTCTGGGGATTAAGTTTGACCCCGCTTTAAACACATTCATGATATATGATGTC 50271  
Qy 463 GAGCAGTGGAAACACGCTACAGCATGCGCGCGCCCGCCAGTCCACGAGCGATTTATGGAC 522  
Db 50270 GAAACACAGAGCCGCTTAATGGAGATGATACC-----CGTTTGCMACT 50223  
Qy 523 GCATCACCGCCCGCGGACCGGTATCATCGTTCTGGGTCTGACCCCGGAGCCCATCGC 582  
Db 50222 GCAACACGACCGCTTGGTACCGTTTACTTTGCGATGTCCCGATGTCCGATGTGGAAGG 50163  
Qy 583 GTCCCGTTTACGCTTACGGCAGCGCGGAGTACTTTTACATGAACGCGGAGGTGGAT 642  
Db 50162 GTGGCAGTTTATGATACGGCATCTGTCAATATTTTATATAAACAAAGCCGAGGTGGAT 50103

Qy 643 CGGCACCTCGAGTGCCTGCCCGCGCGATCTCTGGAGCGCTGCGCGG----- 693  
Db 50102 ACGCTTGTGGCATAGTTCCGGTAGCGAGTTATCTGTATTACTTGCAGGTGTTTACGC 50043  
Qy 694 -----GCCCTGCGGAGTCCGCGGG 714  
Db 50042 AGTTCTATGATAACAAATGATGCAAGCTTTAAATGGAGACAAGAACGCTTTTCATGGT 49983  
Qy 715 GGTGCTTCCCGGGCATCTCCGGGACCACTTCGAGCGGAGGTGCTGGAGCGCGCGAC 774  
Db 49982 ACCTCGTTTAAAGCGCATCTCCAGAAAGCTTTCCGGTGTGAGGTATGAGCGCACAGAT 49923  
Qy 775 GTGTACTATTAGAAACGCGCCCGACCCCTGTACTACCGGCTCTTCGTGGGAAGCGGCGC 834  
Db 49922 GTTTATTACTACGATACAGCATGTGCGTTTACAGGGTGTATTCTCCCTCATCTAAA 49863  
Qy 835 GCGTGGCCTACTGTGCGACAACTTTTGGCCCGCATCAGGAAGTACGAGGGGGCGTC 894  
Db 49862 TTTACAAAATTATCTTTGTGATAACTTTTCAACCGGAGTTGAAAAAGTATGAAGCTCGGTA 49803  
Qy 895 GAGCCACCAACCGGTTTATCCTGGACAAACCGGGGTTTGTACCTTCGGCTGGTACCGC 954  
Db 49802 GAGCTACCACCTCGTTTCTAATGATAATCCCGGCTTTGTAGTTTGGTTGGTATCAA 49743  
Qy 955 CTCAAGCCCGCGCGGAAACGCGCGCCCAACCGCGCCCGCCCGACGCGTTTCGGAACC 1014  
Db 49742 CTAAACCTGGAGTTGATGGGAAACGTGTTCGAGTTTCGACCGGCAAGTCCCAATTTAACG 49683  
Qy 1015 TCGAGCGAGCTGAGTTTAACTGACGCGGCAACACTCGCGCGTCGAGGGGGCCATGTGT 1074  
Db 49682 TTAAGCGAGTTTGAATTTGACTGTCATGTCGGATAATCTCGAGGCTATACCAACGATGAC 49623  
Qy 1075 GACCTGCGCGCTACAAGCTCATGCTTCGATATCGAATCAAGCCCGGGGGAGGAC 1134  
Db 49622 TCATGCGCTGACTACAAGTTGTTATGTTTCGATAITGAATGAAATCAGAGAGTCTAAT 49563  
Qy 1135 GAGCTGGCCTTTCCGTCGCGGAACGCCCGGAAGACCTCGTCATCAGATCTCTCTCTG 1194  
Db 49562 GAGCTGGCCTTTCCGATGCAACACATCTGGAGGATCTTGTATCCAAATTTCTGTCTA 49503  
Qy 1195 CTCTACGAGCTGTCCACACCCCTCGAGCAATCCTCTCTGTTTTCGCTGGATCCTGC 1254  
Db 49502 TTATATTCAATCCCTCGACAGTCTTTAGAACACATTTTACTGTTTCCCTTGGCTTGT 49443  
Qy 1255 GACCTCCCGAGTCCCACTCAGCGATCTCGCTCAGGGGCTCGCGCCCGCCGCTC 1314  
Db 49442 GACTTACCACAAAGTATGTAACAAGATGAAGGACGCGGGTTACCGAGCGCACTGTG 49383  
Qy 1315 CTGGAGTTTGACAGCGAATTCGAGATGCTGCTGGCCTTCATGACCTTCGTCAAGCAGTAC 1374  
Db 49382 CTGGAGTTTGATGTAATTCGAGCTATTAAATTGCAATTTATGACCTCGTAAACAGTAC 49323  
Qy 1375 GGCCTCGAGTTCTGACCGGGTACAAATCATCATCTTCGACTGGCCCTTCGTCCTGACC 1434  
Db 49322 GCTCCCGAGTTTGGCACAGGTTATAACATTTGTAATTTGATTTGGCGTTTATTATGGAG 49263  
Qy 1435 AAGCTGACGAGATCTACAAGTCCGCTCGAGGAGTACGGGCGATGAACGCGCGGGT 1494  
Db 49262 AAACTTAATCTTATATACAGTCTCAAGCTTGTGTTATGGCAGTATAAACCGTGGGGGT 49203  
Qy 1495 GTGTTCCCGCTGGGACATCGCCAGAGCCACTTTTCAGAAGCGCAGCAAGATCAAGGTG 1554  
Db 49202 CTGTTTAAAGATATGGATCTTGGCAATCCCGATTTTCAGCAGCAAGCAAGTAAAGATC 49143  
Qy 1555 AACGGATGGTGAACATCGACATGTACGGCATCATCACGCAAGAGTCAAACTCTCCAGC 1614  
Db 49142 AACGGTCTCATCTCTCGATATGTATGCAATTTGCAATTTGCAATTTAAATACTCTGAGT 49083  
Qy 1615 TACAAGTCAAGCGCTGCCCGAGCCGCTTTGAGAGCAAGAAAGAGATCTGAGTAC 1674  
Db 49082 TATNAATTAGATTTCGGTTCGACGTAAGCTCTAAATGAGTCCAAGAGAGATTTGCCCTAC 49023  
Qy 1675 CGCGACATCCCGCCCTACTACGCTCCGGGCCCGCGCAGCGGGGTGATCGCGGAGTAT 1734

Db	49022	AAAGACATTCGGGATATTTACCTAGTGGACCAATATACAGGAGAAATATTGGTGAATAT	48963
Qy	1735	TGTGTGCAAGACTCGCTGCTGTGGCGAGCTGTCTTCAAGTCTTTCGCGCACCTGGAG	1794
Db	48962	TGTATACAAGACTCGCTCTTGTGGGAAACTGTTTTTAATATATTACCACACCTTGAG	48903
Qy	1795	CTTTCCGCGCTCGCGCGCTGGCGGCATCAACATACACCGCACCATCTACGACGGCCAG	1854
Db	48902	TTATCCGCGGTTGCAAGGCTAGTAGAATTTACTTTAAACCAAGGCTATTATTACGACGGACAG	48843
Qy	1855	CAGATCCGCTCTTCACTGCTCTCGCTGCGCTTGGCGGCAAGAGGGCTTCATCTGCGG	1914
Db	48842	CAGGTTAGGATTTACACCTGTTTATTTAGGACTGGCTTGTCTCGAGGATTTATTTTACCC	48783
Qy	1915	GACACCCAGGGCGGTTTCGGGCGCTTCGACAAAGAGAGGGCGCCCAAGCGCCCGCGCTGCGCT	1974
Db	48782	GATGGGGATACCCAGCTACTTTTGAATATAGGATGTTATTCC-----	48739
Qy	1975	CGGGGGGAAGGGGAGCGGCGCGGGGACGGGAAACGGGGACGAGGATAAGACACGACGAG	2034
Db	48738	-----CGATGTCGGGATGTTGAGGAA	48717
Qy	2035	GACGAGGACGGGACGAGCGCGAGGAGTTCGCGCGAGACCGGGCGCGCACCTTGGG	2094
Db	48716	GAGATGGATGAAGACGAGAGCGTTTCTCCACTGTGATCGTCAAGTGGGGAATGTAGAA	48657
Qy	2095	TACCAAGGGGCGCGGTCTCGACCCCACTCCGGGTTTTCAGTCTGACCCCGTGGTGGTG	2154
Db	48656	TATAAAGGAGCCAGGTTTTCGACCTTGATACGGGATTTATATCGATCCGGTGGTGTGA	48597
Qy	2155	TTTGACTTTGCGAGCTGTACCCAGCATCATCCAGGCCACAACTGTGCTTCAGTAGG	2214
Db	48596	TTGGATTTTGAAGTTTATATCAAGTATAATTTCAGGGCCATAACTTATGTTTTCACACG	48537
Qy	2215	CTCTCCCTCGCGCGAGCGCTCGCGACCTTGAGGGGCGCGGACTACCTGGAGATC	2274
Db	48536	CTAACGTTAAATTTTGAACGGTTTAAACGTTTGAATCCATCC---GATTATGCCACCTTT	48480
Qy	2275	GAGGTGGGGGCGCAGCGGTGTTCTTGTGAAGGCCCAAGTACGGGAGAGCCTGCTGAGC	2334
Db	48479	ACAGTTGGAGGAAACGTCCTTTTTTTTGTGCGCTCTAAGTTTCGAGAAAGTCTGCTGGGT	48420
Qy	2335	ATCTGCTCGCGCATGCGGTGCGCATGCGAAAGCAGATCCGCTCGGGATCCCCAGAGC	2394
Db	48419	GTTCTTTTAAAGACATGGTTGGCTATGCGCAAGGGCTATTAGAGCGCGCATACCCGGAAAT	48360
Qy	2395	ACCCCGGAGGCGCTCCTCTCGACAAAGCAACAGCGCGCATCAAGTGGTGTGCAAC	2454
Db	48359	TCTTCAGATGAAGCAGTGTATTAGACAAACAAAGCCCGCATAAAGTAGTGTGTAAAT	48300
Qy	2455	TCGGTGTACGGTTTACCGGGGCGCAGCAGCTTCTTGCCCTGCTGCACTGGCCGCC	2514
Db	48299	TCGGTGTACGGTTTACTGAGTTGCGCAGGATTTCTGCCATGTTTATACGTAGCGGCC	48240
Qy	2515	ACCGTGACGACCATCGGCGCGAGATGCTCCTCGCGACCGCGCGCTACGTGCAACGCGGC	2574
Db	48239	ACTGTCACTACAAATTTGGCGCTCAAAATGTTATTAAAGTACCAGAGATTATATTCAATAAAC	48180
Qy	2575	TGGGCGGAGTTCCGATCAGCTGTGCGCACTTTTCCGGA---GGCGCGGCATGCGCGCC	2631
Db	48179	TGGGCGCATTTGAAGTTTATTATACAGGTTTTCCAGACATTTGAAGTAGCGTTCTCTCC	48120
Qy	2632	CCCGGTTCGTACTCCATCGCATCATCTACGGGGACAGGACTCCATTTTGGTTGTGC	2691
Db	48119	CAAAAAGCGTACGAGTAAAGGTTATATATGGAGATACGGATTCCTGTGTTATCCGATTC	48060
Qy	2692	CGCGGCTCACGGCGCGCGCTGTGGCATGCGGACAAAGATGGCGGACCATCTCG	2751
Db	48059	AAGGGTGTAGTGTGTAGGGGATAGCTAAAAATCGCGGAAAAATGGCACATATAATTCA	48000
Qy	2752	CGCGGCTGTTCTCTCCCGCGATCAAGCTTCGAGTCGAAAAAACGTTACCAAGCTGCTG	2811

Search completed: August 6, 2005, 09:57:55

Job time : 598 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	3717	100.0	3717	6	AR454707	AR454707 Sequence
2	3717	100.0	3717	6	AX358310	AX358310 Sequence
3	3696.2	99.4	3723	6	AR454708	AR454708 Sequence
4	3696.2	99.4	3723	6	AX358312	AX358312 Sequence
5	3696.2	99.4	3723	14	AY038367	AY038367 Human herpesvirus 1
6	3694.6	99.4	3723	14	AY038366	AY038366 Human herpesvirus 1
7	3693	99.4	154746	14	H5V2HG52	H5V2HG52 Herpes simplex virus 1
8	3686.6	99.2	4003	14	H52POL	M16321 HSV-2 DNA polymerase
9	3059.8	82.3	3708	6	AR454709	AR454709 Sequence
10	3059.8	82.3	3708	6	AX358314	AX358314 Sequence
11	3059.8	82.3	3708	14	AB070847	AB070847 Human herpesvirus 1
12	3058.2	82.3	3708	14	AB070848	AB070848 Human herpesvirus 1
13	3056.6	82.2	4435	14	H51POL	M10792 Herpes simplex virus 1
14	3053.4	82.1	3708	6	AR454710	AR454710 Sequence
15	3053.4	82.1	3708	6	AX358316	AX358316 Sequence
16	3053.4	82.1	3708	14	HEHSVDP	X04771 Herpes simplex virus 1
17	3048.6	82.0	3708	14	AB072389	AB072389 Human herpesvirus 1
18	3048.6	82.0	152261	14	HE1CG	X14112 Human herpesvirus 1
19	3047	82.0	3708	6	AR454711	AR454711 Sequence

Db 241 CGTTCTGTCAGAGAGCGCCCCCGCGGAGACGCGCACCGGGGTCCACGACGCGCGCTC 300  
QY CGCGCGCCCTTAAGGTGTACTGCGGGGGGAGCGAGCGCAGCTCTCCCGCTGGGCGCG 360  
Db 301 CGGCGCCCTTAAGGTGTACTGCGGGGGGAGCGAGCGCAGCTCTCCCGCTGGGCGCG 360  
QY 361 GAGGCTTCTGGCGCGCTCGCTTGGCGCTGTGGGGCGGTGCGGACCATGCCCCAAGGGG 420  
Db 361 GAGGCTTCTGGCGCGCTCGCTTGGCGCTGTGGGGCGGTGCGGACCATGCCCCAAGGGG 420  
QY 421 TTGACCCCAACCGTCAACCGTCTTCCAGCTGTACGACATCTCTGAGACGCTGGAACACGCG 480  
Db 421 TTGACCCCAACCGTCAACCGTCTTCCAGCTGTACGACATCTCTGAGACGCTGGAACACGCG 480  
QY 481 TAGACATGCGCGCGCCAGCTCCAGAGCGATTTATGACGCGCATACGCGCGCGCGG 540  
Db 481 TACAGCATGCGCGCGCCAGCTCCAGAGCGATTTATGACGCGCATACGCGCGCGCGG 540  
QY 541 ACCGTCAACAGCTTCTGGGTCTGACCCCGAAGGCCATCGCGTCGCGTTACGCTTAC 600  
Db 541 ACCGTCAACAGCTTCTGGGTCTGACCCCGAAGGCCATCGCGTCGCGTTACGCTTAC 600  
QY 601 GGACGCGGAGTACTTTTACATGAACAAGCGGAGGTGATCGGCACCTGCGAGTGCCTG 660  
Db 601 GGACGCGGAGTACTTTTACATGAACAAGCGGAGGTGATCGGCACCTGCGAGTGCCTG 660  
QY 661 GCCCGCGCGATCTCTCGAGCGCTGCGCGCGCGCCCTGCGAGTCCGCGGGGGGTG 720  
Db 661 GCCCGCGCGATCTCTCGAGCGCTGCGCGCGCGCCCTGCGAGTCCGCGGGGGGTG 720  
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Db 781 TATTACGAAGCGCGCGACCTGTACTACGGGTCTTCTGTGCGAGCGCGCGCGCTG 840  
QY 841 GCCTACTGTGCGACAACTTTTGCCCGCGATCAGGAAGTACGAGGGGGCGTTCGAGCC 900  
Db 841 GCCTACTGTGCGACAACTTTTGCCCGCGATCAGGAAGTACGAGGGGGCGTTCGAGCC 900  
QY 901 ACCACCGGTTTATCTGGACAACCCCGGGTGTGTACCTTCGCTGGTACCGCTCAAG 960  
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QY 961 CCGCGCGCGGGAACGCGCGCGCGCCAAACCGCGCGCGCGTTCGGAACCTCGAGC 1020  
Db 961 CCGCGCGCGGGAACGCGCGCGCGCCAAACCGCGCGCGCGTTCGGAACCTCGAGC 1020  
QY 1021 GAGTCTGAGTTTAACCTGACGCGGACAACTTGCGCTGAGGGGCGATGTGTACCTG 1080  
Db 1021 GAGTCTGAGTTTAACCTGACGCGGACAACTTGCGCTGAGGGGCGATGTGTACCTG 1080  
QY 1081 CCGGCTTACAGCTCATGTCTCGATATCGAATGCAAGCGCGGGGGAGGACGAGCTG 1140  
Db 1081 CCGGCTTACAGCTCATGTCTCGATATCGAATGCAAGCGCGGGGGAGGACGAGCTG 1140  
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QY 1261 CCGAGTCCACCTCTCAGCATCTGCGCTTCAGGGGCTGCGCGCGCGCTGCTGTGAG 1320  
Db 1261 CCGAGTCCACCTCTCAGCATCTGCGCTTCAGGGGCTGCGCGCGCGCTGCTGTGAG 1320  
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Db 1321 TTTGACAGCGAATTCGAGATGCTGCGCTTACATGACCTTCGTCAGCAGTACGCGCC 1380

QY 1381 GAGTTCGTGACCGGGTACAACATCATCAACTTCGACTGGCCCTTCGTCTCTGACCAAGCTG 1440  
Db 1381 GAGTTCGTGACCGGGTACAACATCATCAACTTCGACTGGCCCTTCGTCTCTGACCAAGCTG 1440  
QY 1441 ACGAGATCTACAAGTTCGCTCGAGCGGTACGGGCGCATGAACCGCGCGGGTGTTC 1500  
Db 1441 ACGAGATCTACAAGTTCGCTCGAGCGGTACGGGCGCATGAACCGCGCGGGTGTTC 1500  
QY 1501 CGGCTGTGGACATCGGCGAGGACCTTTTCAGAGCGCAGCAAGATCAAGGTGAACGG 1560  
Db 1501 CGGCTGTGGACATCGGCGAGGACCTTTTCAGAGCGCAGCAAGATCAAGGTGAACGG 1560  
QY 1561 ATGGTGAACATCGACATGTACGCGCATCATCACGACAAAGTCAAACTCTCCAGCTACAAG 1620  
Db 1561 ATGGTGAACATCGACATGTACGCGCATCATCACGACAAAGTCAAACTCTCCAGCTACAAG 1620  
QY 1621 CTGAACCGCTCGCGAGGCGCTTTTGAAGGACAGAAAGGATCTGAGCTACCGGAC 1680  
Db 1621 CTGAACCGCTCGCGAGGCGCTTTTGAAGGACAGAAAGGATCTGAGCTACCGGAC 1680  
QY 1681 ATCCCGCTTACTACGCTCTCGGCGCGCGAGCGGGGTGATCGGCGAGTATTCGTG 1740  
Db 1681 ATCCCGCTTACTACGCTCTCGGCGCGCGAGCGGGGTGATCGGCGAGTATTCGTG 1740  
QY 1741 CAGGACTCGCTGCTGGTGGGCGAGCTTTCTTCAAGTTTCTGCGCACTCTGAGCTTTTC 1800  
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Db 1801 GCGCTCGCGCTGCGGGCATCAACATCAACCGCACTCTTACGACGCGCGAGCAGATC 1860  
QY 1861 CCGCTCTTCACTGCTGCTGCGCTTTCGCGCGCAGAGGGCTTCATCTGCGGACACC 1920  
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Db 1921 CAGGGCGGTTTCGCGGCTTCGACAGAGGGGCGCCCAAGCGCGCGCGCTGCTCGGGG 1980  
QY 1981 GAAGGGGAGCGGCGCGGGGACCGGGAACCGGGACGAGGATGAAGACGACGAGGACGAG 2040  
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QY 2041 GACGGGAGCAGCGCGAGGAGGTGCGCGCGAGACCGGGGCGCGCACGTTGGGTACCAG 2100  
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Db 2101 GGGGCGCGGCTCTCTGACCCCGCTTCAGCTCGACCGCTGGTGGTGGTGGTGGTGGT 2160  
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QY 2401 GAGGAGCGCTCTCTCTCGACAAAGCAACAGGCGCGCATCAAGGTGGTGTGCAACTCGGTG 2460  
Db 2401 GAGGAGCGCTCTCTCTCGACAAAGCAACAGGCGCGCATCAAGGTGGTGTGCAACTCGGTG 2460





Db ||||| 481 TACAGCATGCGCGCCAGCTCCACGAGCATTTATGACGCCATCACGCCCGCGGG 540  
Qy ||||| 541 ACCGTATACGCTTCTGGTCTGACCCCGAGGCCATCGCTCGCGTTCACTCTAC 600  
Db ||||| 541 ACCGTATACGCTTCTGGTCTGACCCCGAGGCCATCGCTCGCGTTCACTCTAC 600  
Qy ||||| 601 GGACGCGGAGTACTTTTATGAAACAGCGAGGTGATCGGCACTTCACTGCGCT 660  
Db ||||| 601 GGACGCGGAGTACTTTTATGAAACAGCGAGGTGATCGGCACTTCACTGCGCT 660  
Qy ||||| 661 GCCCGCGCATCTCTCGAGCGCTGCGCGCGCCCTGCGAGTCCGCGGGGCGTGC 720  
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Qy ||||| 721 TTCCGCGCATCTCCGCGACCACTTCGAGCGGAGGTGATGAGCGCGCGAGTGTAC 780  
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Qy ||||| 781 TATTACGAACGCGCCGACCTCTGACTACCGGTCTTCTGCGAAGCGGCGCGCTG 840  
Db ||||| 781 TATTACGAACGCGCCGACCTCTGACTACCGGTCTTCTGCGAAGCGGCGCGCTG 840  
Qy ||||| 841 GCCTACTGTGCGCAACTTTTGTCCCGCGATCAGGAAGTACGAGGGGGCGTCGAGCC 900  
Db ||||| 901 ACCACCGGTTATCTGGACAACCCCGGGTTTGTGACTTCCGCTGGTACCGCTCAAG 960  
Qy ||||| 901 ACCACCGGTTATCTGGACAACCCCGGGTTTGTGACTTCCGCTGGTACCGCTCAAG 960  
Qy ||||| 961 CCCGGCGCGGAACCGCGCCCAACCGCGCCCGCGCGCTTCCGAACTCTGAGC 1020  
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Qy ||||| 1021 GAGTGCAGTTTAACTGCAAGCGGCAAACTGCGCTCGAGGGGGCCATGTGACCTG 1080  
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Qy ||||| 1081 CCGGCTTACAGCTCATGTCTCGATATCGAATGCAAGCGCGGGGGAGGACGAGCTG 1140  
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Qy ||||| 1141 GCCTTTCGGTTCGCGAAGCGCGGAGAACTCTGTCATCCAGATCTCTCTGCTCTAC 1200  
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Qy ||||| 1201 GACTGTCCACCGCCCTCGAGCAATCTCTCTGTTTTCGCTCGGATCTCTGCGACCTC 1260  
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Qy ||||| 1321 TTGTACAGCGAATTCGAGATGCTCTGCGCTTATGACCTTCTGTCAGAGTACGCGCC 1380  
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Qy ||||| 1381 GAGTTCGTGACCGGGTCAACATCATCAACTTCGACTGGGCTTCTGCTCGACCAAGCTG 1440  
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Qy ||||| 1441 ACGAGATCTACAGGTCCCGCTCGAGGTACGGGCGCATGAACGCGGGGTGTTTC 1500  
Db ||||| 1441 ACGAGATCTACAGGTCCCGCTCGAGGTACGGGCGCATGAACGCGGGGTGTTTC 1500  
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ACCESSION AX358312
VERSION AX358312.1 GI:18674961
KEYWORDS
SOURCE Human herpesvirus 2 strain 186
ORGANISM Human herpesvirus 2 strain 186
VIRUSES; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
REFERENCE
1 Homa, F.L., Wathen, M.W., Hopkins, T.A. and Thomeen, D.R.
AUTHORS A method for treating herpes viruses
TITLE
JOURNAL PHARMACIA & UPJOHN COMPANY (US)
FEATURES
Location/Qualifiers
source
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ORIGIN

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VERSION	AY038367.1	GI:14860974	
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SOURCE	Human herpesvirus 2		
ORGANISM	Human herpesvirus 2		
REFERENCE	1		
AUTHORS	Alphaherpesvirinae; Simplexvirus.		
TITLE	Novel mutations in the thymidine kinase and DNA polymerase genes of acyclovir and foscarnet resistant herpes simplex viruses infecting an immunocompromised patient		
JOURNAL	J. Clin. Virol. 25 (2), 165-170 (2002)		
MEDLINE	22254960		
PUBMED	12367650		
REFERENCE	2		
AUTHORS	Chibo, D., Mich, A., Doherty, R. and Birch, C.J.		
TITLE	Submitted (04-JUN-2001) Viral Identification, Victorian Infectious Diseases Reference Laboratory, 10 Wreckyn St, Melbourne, Victoria 3051, Australia		
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RTSRALVDLLFYDDTVSAAAALAEERPAEHLARPLPEGLQAFGLVLDHRRITDPE  
RQDFVLITAELSRHRPNTKRLAHITVYKLMARRAQVPSIKDRIPYVIAQTRV  
EETVARLAURELDAAPDEPPAPALPSAKRPRETPSHADPPGASPKRLVSE  
LAEDPGYAIARGVPLNTDYFVSHLLGAACVTFKALFGNNAKITESLLKRFIPETWHPP  
DDVAARLRAAGFPAGAGATAETRRMLHRAFDLA"

## ORIGIN

Query Match	99.4%	Score	3696.2	DB	14	Length	3723
Best Local Similarity	99.8%	Pred. No.	0				
Matches	3714	Conservative	0	Mismatches	3	Indels	6
Gaps	1						
Qy	1	ATGTTTGTGCGCGCGCGCGCGCGCTTCCCGGGGGAGTCCGCGCGCTCGCGCGCGCG	60				
Db	1	ATGTTTGTGCGCGCGCGCGCGCGCTTCCCGGGGGAGTCCGCGCGCTCGCGCGCGCG	60				
Qy	61	TCTGGGTTTTTGTGCG	120				
Db	61	TCTGGGTTTTTGTGCG	120				
Qy	121	CG	180				
Db	121	CG	180				
Qy	181	GGCGCGCGCTCAGCG	240				
Db	181	GGCGCGCGCTCAGCG	240				
Qy	241	CGTTTCGTGAGCGAGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	300				
Db	241	CGTTTCGTGAGCGAGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	300				
Qy	301	CG	360				
Db	301	CG	360				
Qy	361	GAGGGCTTCTGCG	420				
Db	361	GAGGGCTTCTGCG	420				
Qy	421	TTGACCG	480				
Db	421	TTGACCG	480				
Qy	481	TACAGCATGCG	540				
Db	481	TACAGCATGCG	540				

Qy	541	ACGTCATACGCTTCTGGGTCTGACCCCGAAGGCCATCGCTCGCGCTTACGCTCTAC	600	Qy	1621	CTGAACCGCGTCCCGAGGCCGCTTTGAAGGACAAAGAAAGGATCTGAGTACCGCGAC	1680
Db	541	ACGTCATACGCTTCTGGGTCTGACCCCGAAGGCCATCGCTCGCGCTTACGCTCTAC	600	Db	1621	CTGAACCGCGTCCCGAGGCCGCTTTGAAGGACAAAGAAAGGATCTGAGTACCGCGAC	1680
Qy	601	GGCAGCGGAGTACTTTTATCATGAACAAGCGGAGGTGGATCGGCACTTCGAGTGCCTG	660	Qy	1681	ATCCCGCGCTACTACGCCCTTCGGGCCCGGACGCGGGGTGATCGCGAGTATTTGTGTG	1740
Db	601	GGCAGCGGAGTACTTTTATCATGAACAAGCGGAGGTGGATCGGCACTTCGAGTGCCTG	660	Db	1681	ATCCCGCGCTACTACGCCCTTCGGGCCCGGACGCGGGGTGATCGCGAGTATTTGTGTG	1740
Qy	661	GCCCGCGGATCTCTCGAGAGCGCTTCGCGCGGCGCTTCGCGAGTTCGCGGGGCGTGC	720	Qy	1741	CAGGACTCGCTGCTGGTTCGGGAGCTGTTCTTCAAGTTTCTGCGCACCTGGAGCTTTTC	1800
Db	661	GCCCGCGGATCTCTCGAGAGCGCTTCGCGCGGCGCTTCGCGAGTTCGCGGGGCGTGC	720	Db	1741	CAGGACTCGCTGCTGGTTCGGGAGCTGTTCTTCAAGTTTCTGCGCACCTGGAGCTTTTC	1800
Qy	721	TTCCGCGGATCTCCCGGAGCACTTCGAGCGGAGGTGTGGAGCGCGCCGACGTGTAC	780	Qy	1801	GCCGTCCGCGCGCTTCGGGCGCATCAACATACCCGCCACCATCTACGACGCGCAGCAGATC	1860
Db	721	TTCCGCGGATCTCCCGGAGCACTTCGAGCGGAGGTGTGGAGCGCGCCGACGTGTAC	780	Db	1801	GCCGTCCGCGCGCTTCGGGCGCATCAACATACCCGCCACCATCTACGACGCGCAGCAGATC	1860
Qy	781	TATTAAGAAACGCGCCGACCTGTACTACCGGTCTTCTGCGAAGCGGCGCGGCTG	840	Qy	1861	CGGCTTTTCACTGCTCTCGGCTTCGGGCGCAGAGGCTTCACTCTGCCGGAACACC	1920
Db	781	TATTAAGAAACGCGCCGACCTGTACTACCGGTCTTCTGCGAAGCGGCGCGGCTG	840	Db	1861	CGGCTTTTCACTGCTCTCGGCTTCGGGCGCAGAGGCTTCACTCTGCCGGAACACC	1920
Qy	841	GCCTACTGTGCGACAACTTTTGGCCCGCGATCAGGAAGTACGAGGGGCGCTGACGCC	900	Qy	1921	CAAGGCGGTTTTCGGGCGCTTCGACAGAGAGGCGCCCAAGCGCCCGCTGCTCGGGG	1980
Db	841	GCCTACTGTGCGACAACTTTTGGCCCGCGATCAGGAAGTACGAGGGGCGCTGACGCC	900	Db	1921	CAAGGCGGTTTTCGGGCGCTTCGACAGAGAGGCGCCCAAGCGCCCGCTGCTCGGGG	1980
Qy	901	ACCACCGGTTTATCTTGGACAAACCGGGGTTTGTCACTTCGGCTGGTACCGCTCAAG	960	Qy	1981	GAAGGGAGCGGCGCGGGGACGCGGAAACGAGGATAAGGACGACGACGCGA-----G	2034
Db	901	ACCACCGGTTTATCTTGGACAAACCGGGGTTTGTCACTTCGGCTGGTACCGCTCAAG	960	Db	1981	GAAGGGAGCGGCGCGGGGACGCGGAAACGAGGATAAGGACGACGACGCGGACGCGG	2034
Qy	961	CCGCGCGCGGGAACGCGCGCGGCGCAACCGCGCCCGCGACGCGGCTTCGGAACCTCGAGC	1020	Qy	2035	GACGAGGACGCGGACGAGCGCGAGGAGTTCGCGCGGAGACCGGGGCGCGGACGTTGGG	2094
Db	961	CCGCGCGCGGGAACGCGCGCGGCGCAACCGCGCCCGCGACGCGGCTTCGGAACCTCGAGC	1020	Db	2041	GACGAGGACGCGGACGAGCGCGAGGAGTTCGCGCGGAGACCGGGGCGCGGACGTTGGG	2100
Qy	1021	GAGTCTCAGTTTAACTGCAAGCGGCAAACTTGGCTTCGAGGGGCGATGTGACCTG	1080	Qy	2095	TACACGCGGCGCGGCTTCGACCCACCTCGGGTTTCACTCGACCCGCTGGTGGT	2154
Db	1021	GAGTCTCAGTTTAACTGCAAGCGGCAAACTTGGCTTCGAGGGGCGATGTGACCTG	1080	Db	2101	TACACGCGGCGCGGCTTCGACCCACCTCGGGTTTCACTCGACCCGCTGGTGGT	2160
Qy	1081	CCGGCTTACAGCTCATGTGCTTCGATATCGAATGCAAGCGCGGGGAGGACGAGCTG	1140	Qy	2155	TTTGAATTTGCCAGCTGTACCCAGCATCATCCAGGCCCAACCTGTGCTTCAAGTACG	2214
Db	1081	CCGGCTTACAGCTCATGTGCTTCGATATCGAATGCAAGCGCGGGGAGGACGAGCTG	1140	Db	2161	TTTGAATTTGCCAGCTGTACCCAGCATCATCCAGGCCCAACCTGTGCTTCAAGTACG	2220
Qy	1141	GCCTTTCGGTTCGCGAAGCGCGCGGAAAGCTCTGTCATCCAGATCTCTGCTCTAC	1200	Qy	2215	CTCTCCTCGGCGCGGCGCTTCGCGCACCTTGAGGCGGACCGGGACCTACCTGGAGATC	2274
Db	1141	GCCTTTCGGTTCGCGAAGCGCGCGGAAAGCTCTGTCATCCAGATCTCTGCTCTAC	1200	Db	2221	CTCTCCTCGGCGCGGCGCTTCGCGCACCTTGAGGCGGACCGGGACCTACCTGGAGATC	2280
Qy	1201	GACCTGTCCACCGCGCTCGAGCATCTCTCTGTTTTCGCTCGGATCCTCGGACCTC	1260	Qy	2275	GAGTGGGGGCGACGCGCTTCTTCTGTAAGGCCCACTGACGAGAGCTCTGCTGAGC	2334
Db	1201	GACCTGTCCACCGCGCTCGAGCATCTCTCTGTTTTCGCTCGGATCCTCGGACCTC	1260	Db	2281	GAGTGGGGGCGACGCGCTTCTTCTGTAAGGCCCACTGACGAGAGCTCTGCTGAGC	2340
Qy	1261	CCGAGTCCCACTCAGCGATCTCGCTTCAGGGGCGCTCGCGCCCGCTCGCTCGGAG	1320	Qy	2335	ATCCTGCTCGGCACTGGCTGGCCATGCGAAGACAGATTCGCTCGCGGATTCGCCAGAGC	2394
Db	1261	CCGAGTCCCACTCAGCGATCTCGCTTCAGGGGCGCTCGCGCCCGCTCGCTCGGAG	1320	Db	2341	ATCCTGCTCGGCACTGGCTGGCCATGCGAAGACAGATTCGCTCGCGGATTCGCCAGAGC	2400
Qy	1321	TTTGAAGCGAATTCGAGATGCTGCTGGCTTTCATGACCTTCGTCGAGCAGTACGGCCCC	1380	Qy	2395	ACCCCGAGGAGCGCTCTCTCGACAAACACAGCGCGCCCATCAAGTGGTGTGCAAC	2454
Db	1321	TTTGAAGCGAATTCGAGATGCTGCTGGCTTTCATGACCTTCGTCGAGCAGTACGGCCCC	1380	Db	2401	ACCCCGAGGAGCGCTCTCTCGACAAACACAGCGCGCCCATCAAGTGGTGTGCAAC	2460
Qy	1381	GAGTTCGTGACCGGGTACACATCACTTCGACCTGCGCTTCGCTCGACCAAGCTG	1440	Qy	2455	TCGCTGTACGGGTTACCGGGGCGACACGCTTCTTCTGCTCTGCTCGCTGCACTGGCGCC	2514
Db	1381	GAGTTCGTGACCGGGTACACATCACTTCGACCTGCGCTTCGCTCGACCAAGCTG	1440	Db	2461	TCGCTGTACGGGTTACCGGGGTCGACACGCTTCTTCTGCTCTGCTCGACCTGGCGCC	2520
Qy	1441	ACGAGATCTACAGGTCCCGCTCGACGGGTACGGGCGCATGAAACGCGGGGTTGTTTC	1500	Qy	2515	ACCGTGAACACCATCGGCGCGGAGTGTCTCTCGACGCGCGCGGTACGTGACGCGCGC	2574
Db	1441	ACGAGATCTACAGGTCCCGCTCGACGGGTACGGGCGCATGAAACGCGGGGTTGTTTC	1500	Db	2521	ACCGTGAACACCATCGGCGCGGAGTGTCTCTCGACGCGCGCGGTACGTGACGCGCGC	2580
Qy	1501	CGCGTGGGACATTCGCGCAGAGCACTTTCAAGCGCGACAGATCAAGGTGAACGGG	1560	Qy	2575	TGGGCGGAGTTGATCAGCTGTGCGGCTTTCGAGAGCGCGCGCATGCGCGCCCGC	2634
Db	1501	CGCGTGGGACATTCGCGCAGAGCACTTTCAAGCGCGACAGATCAAGGTGAACGGG	1560	Db	2581	TGGGCGGAGTTGATCAGCTGTGCGGCTTTCGAGAGCGCGCGCATGCGCGCCCGC	2640
Qy	1561	ATGGTGAACATTCGACATGTAGGCACTATCACCGCAAGGTCAACCTCTCCAGTCAAG	1620	Qy	2635	GGTCCGCTACTCCATGGCGCATCATCTACGGGGAACAGGACTTCACTTTTGTGCGCG	2694
Db	1561	ATGGTGAACATTCGACATGTAGGCACTATCACCGCAAGGTCAACCTCTCCAGTCAAG	1620	Db	2641	GGTCCGCTACTCCATGGCGCATCATCTACGGGGAACAGGACTTCACTTTTGTGCGCG	2700
				Qy	2695	GGCCTCAAGCGCGCGGCGCTGTGGCCATGGGCGACAAAGATGGGAGCCACATCTCGCGC	2754

Db	2701	GGCCTC ACGGCCGCGGGCGCTGGTGGCCAT GGCGAC AAGATGGCGAGCCCACTCTCGCGC	2760
Qy	2755	GCCTGTTCTCTCCCCCGGATCAAGCTCGAGTGCAGAAAAACGTTACCAAGAGCTGCTGCTC	2814
Db	2761	GCCTGTTCTCTCCCCCGGATCAAGCTCGAGTGCAGAAAAACGTTACCAAGAGCTGCTGCTC	2820
Qy	2815	ATCCCAAGAAAAAGTATCATCGGCGTCACTCGCGGGGCGAAGATGCTCATCAAGAGGCGTG	2874
Db	2821	ATCCCAAGAAAAAGTATCATCGGCGTCACTCGCGGGGCGAAGATGCTCATCAAGAGGCGTG	2880
Qy	2875	GATCTGGTGGCAAAAAACAATCGCGCGTTTATCAACCGCACCTTCAGAGGCCCTGCTCGAC	2934
Db	2881	GATCTGGTGGCAAAAAACAATCGCGCGTTTATCAACCGCACCTTCAGAGGCCCTGCTCGAC	2940
Qy	2935	CTGCTGTTTATCGACGATACCGTATCCGGAGCGGCCCGCGTGTAGCCGAGCGCCCGCA	2994
Db	2941	CTGCTGTTTATCGACGATACCGTATCCGGAGCGGCCCGCGTGTAGCCGAGCGCCCGCA	3000
Qy	2995	GAGAGTGGCTGGCGCGACCCCTGCCGAGGACTGACAGCGTTCGGGGCCGCTCTCGTA	3054
Db	3001	GAGAGTGGCTGGCGCGACCCCTGCCGAGGAGCTGACAGCGTTCGGGGCCGCTCTCGTA	3060
Qy	3055	GAGCCCATCGGCGCATACCGACCCGGAGAGGAGCATCCAGACCTTGTCTCAGCGCC	3114
Db	3061	GAGCCCATCGGCGCATACCGACCCGGAGAGGAGCATCCAGACCTTGTCTCAGCGCC	3120
Qy	3115	GAATCGACGAGACACCCCGCGCGGTACAACAAAGCGCTTGCGCCACCTTGACGGTGTAT	3174
Db	3121	GAATCGACGAGACACCCCGCGCGGTACAACAAAGCGCTTGCGCCACCTTGACGGTGTAT	3180
Qy	3175	TACAAGTCTATGGCCCGCGCGCGAGTCCCGTTCATCAAGAACCGGATCCCGTACGTG	3234
Db	3181	TACAAGTCTATGGCCCGCGCGCGAGTCCCGTTCATCAAGAACCGGATCCCGTACGTG	3240
Qy	3235	ATCGTGGCCAGACCCCGGAGGTAGAGGACGCTGCGCGGTGGCGCGCCCTCCCGGAG	3294
Db	3241	ATCGTGGCCAGACCCCGGAGGTAGAGGACGCTGCGCGGTGGCGCGCCCTCCCGGAG	3300
Qy	3295	CTAGACGCCCGCGCCCAAGGGAGCAGCCCGCCCCCGCCAGCGGCCTTGCCCTCCCGGCC	3354
Db	3301	CTAGACGCCCGCGCCCAAGGGAGCAGCCCGCCCCCGCCAGCGGCCTTGCCCTCCCGGCC	3360
Qy	3355	AAGGGCCCCCGGAGACGCGTCCGATGCCAACCCCGGGAGCGCGTCCAAGCCCCCG	3414
Db	3361	AAGGGCCCCCGGAGACGCGTCCGATGCCAACCCCGGGAGCGCGTCCAAGCCCCCG	3420
Qy	3415	AAGCTGCTGGTGTCCGAGCTGGCGGAGGATCCCGGGTACGCCATCGCCCGGGGCGTTCG	3474
Db	3421	AAGCTGCTGGTGTCCGAGCTGGCGGAGGATCCCGGGTACGCCATCGCCCGGGGCGTTCG	3480
Qy	3475	CTCAACACGACTATTACTTCTCGCACCTGCTGGGGCGGCGCTGCTGACGTTCAAGGCC	3534
Db	3481	CTCAACACGACTATTACTTCTCGCACCTGCTGGGGCGGCGCTGCTGACGTTCAAGGCC	3540
Qy	3535	CTGTTTGGAAATAACGCAAGATCAACGAGAGTCTGTATAAGAGGTTTATTCGCGAGACG	3594
Db	3541	CTGTTTGGAAATAACGCAAGATCAACGAGAGTCTGTATAAGAGGTTTATTCGCGAGACG	3600
Qy	3595	TGGACCCCCCGGACGAGCTGGCCCGCGGCTCAGGGCCGCGGGTTCGGGCGCGGGG	3654
Db	3601	TGGACCCCCCGGACGAGCTGGCCCGCGGCTCAGGGCCGCGGGTTCGGGCGCGGGG	3660
Qy	3655	GCGGGCGTACGGCGGAGGAAATCTGTCGAATGTTGCATAGAGCCTTTGATCTCTAGCA	3714
Db	3661	GCGGGCGTACGGCGGAGGAAATCTGTCGAATGTTGCATAGAGCCTTTGATCTCTAGCA	3720
Qy	3715	TGA	3717
Db	3721	TGA	3723

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Qy 121 CGCCGCGAGAACTTCTAACAACCCCACTCTGGCTCAGACCGGAAACGACGACCAAGGCCCCC 180  
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Qy 181 GGGCGGCTCAGCCCACTAGTACTA CAGCGAGTGCAGCGAAATTCGATTTATGCGCCCG 240  
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Qy 241 CGTTCCGTGACGAGGAGCCCGCCGCGGAGCGGACCGGGTCCACGAGCGCGCTC 300  
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Qy 241 CGTTCCGTGACGAGGAGCCCGCCGCGGAGCGGACCGGGTCCACGAGCGCGCTC 300  
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Qy 301 CGGCGCGCCCTAAGGTGTACTGCGGGGGGACGAGCGGACGCTCTCCGCTGGGGCCG 360  
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Qy 301 CGGCGCGCCCTAAGGTGTACTGCGGGGGGACGAGCGGACGCTCTCCGCTGGGGCCG 360  
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Qy 361 GAGGGCTTTCGCGCTGCTTGGCTTGGCTGCGGGGCGGTGGGACCAATGCCCCGAAGGG 420  
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Qy 361 GAGGGCTTTCGCGCTGCTTGGCTTGGCTGCGGGGCGGTGGGACCAATGCCCCGAAGGG 420  
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Qy 541 ACCGTCAATACGCTTCTGGGTCTGACCCCGAAGGCCATCGCTGCGCGTTCAGTCTAC 600  
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Qy 2215 CTCTCCCTGCGGCGCGAGGCGCTCGCGCACTTCGAGGCGGACCGGGGACTACCTGAGATC 2274  
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Qy 2221 CTCTCCCTGCGGCGCGAGGCGCTCGCGCACTTCGAGGCGGACCGGGGACTACCTGAGATC 2280  
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Qy 2275 GAGGTGGGGGCGGACGGCTGTTCTTCGTGAAGGCCACCTACGCGAGAGCTCTGCTGAGC 2334  
Db |||||

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Qy	2335	ATCTCTGTCGCGCACTGGCTGGCCCATGCAAAAGCAGATCCCGCTCGCGGATCCCCCAGAGC	2394
Db	2341	ATCTCTGTCGCGCACTGGCTGGCCCATGCGAAGCAGATCCCGCTCGCGGATCCCCCAGAGC	2400
Qy	2395	ACCCCCGAGGAGGGCGTCTCTCTGCAAGCAACAGCGCGCGCATCAAGGTGGTGTGCAAC	2454
Db	2401	ACCCCCGAGGAGGGCGTCTCTCTCGACAAGCAACAGCGCGCGCATCAAGGTGGTGTGCAAC	2460
Qy	2455	TCGGTGTACGGGTTTACCGGGGGCGCAGCAGCGTCTTCTGCCCCCTGCGTGCAGGTGGCGCC	2514
Db	2461	TCGGTGTACGGGTTTACCGGGGGTGAGCAGCGTCTTCTGCCCCCTGCGTGCAGGTGGCGCC	2520
Qy	2515	ACCGTAGCACCATTCGGCGCGGAGATGCTCTCTCGCGACGCGCGGTACGTGCACGCGCGC	2574
Db	2521	ACCGTAGCACCATTCGGCGCGGAGATGCTCTCTCGGACGCGCGGTACGTGCACGCGCGC	2580
Qy	2575	TGGCGGAGTTTCGATTCAGTCTGCTGGCGGACTTTCGAGGCGGCGCGCATGCGCGCCCC	2634
Db	2581	TGGCGGAGTTTCGATTCAGTCTGCTGGCGGACTTTCGAGGCGGCGCGCATGCGCGCCCC	2640
Qy	2635	GGTCCGTACTCCATGCCCATCATCTACGGGGACACGGACTCCATTTTGGTTTGTGCGCG	2694
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VERSION	Z86099.2	GI:6572414	
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REFERENCE	1 (bases 1 to 154746)		
AUTHORS	McGeoch,D.J., Moss,H.W., McNab,D. and Frame,M.C.		
TITLE	DNA sequence and genetic content of the HindIII 1 region in the short unique component of the herpes simplex virus type 2 genome: identification of the gene encoding glycoprotein G, and evolutionary comparisons		
JOURNAL	J. Gen. Virol. 68 (Pt 1), 19-38 (1987)		
MEDLINE	87111457		
PUBMED	3027242		
REFERENCE	2 (bases 1 to 154746)		
AUTHORS	Everett,R.D. and Fenwick,M.L.		
TITLE	Comparative DNA sequence analysis of the host shutoff genes of different strains of herpes simplex virus: type 2 strain HG52		



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encodes a truncated UL41 product
J. Gen. Virol. 71 (Pt 6), 1387-1390 (1990)
MEDLINE 90278430
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REFERENCE 3 (bases 1 to 154746)
AUTHORS McGeoch,D.J., Cunningham,C., McIntyre,G. and Dolan,A.
TITLE Comparative sequence analysis of the long repeat regions and
adjoining parts of the long unique regions in the genomes of herpes
simplex viruses types 1 and 2
J. Gen. Virol. 72 (Pt 12), 3057-3075 (1991)
MEDLINE 92113549
PUBMED 1662697
REFERENCE 4 (bases 1 to 154746)
AUTHORS Barnett,B.C., Dolan,A., Telford,E.A., Davison,A.J. and McGeoch,D.J.
TITLE A novel herpes simplex virus gene (UL49A) encodes a putative
membrane protein with counterparts in other herpesviruses
J. Gen. Virol. 73 (Pt 8), 2167-2171 (1992)
MEDLINE 92356101
PUBMED 1322965
REFERENCE 5
AUTHORS Dolan,A.
TITLE Direct Submission
SUBMITTED (25-FEB-1997) A. Dolan, MRC Virology Unit, Church
Street,, Glasgow,, G11 5JR, UK
REMARK revised bu [6]
AUTHORS Dolan,A.
TITLE Direct Submission
SUBMITTED (08-DEC-1999) A. Dolan, MRC Virology Unit, Church
Street,, Glasgow,, G11 5JR, UK
COMMENT On Dec 13, 1999 this sequence version replaced gi:1869820.
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VERSION			
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AUTHORS			
Tsurumi, T., Maeno, K. and Nishiyama, Y.			
TITLE			
Nucleotide sequence of the DNA polymerase gene of herpes simplex			
virus type 2 and comparison with the type 1 counterpart			
JOURNAL			
Gene 52 (2-3), 129-137 (1987)			
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polya_signal
ORIGIN
887 bp upstream of PstI site; 0.401-0.442 m.u. on genome.

Query Match 99.2%; Score 3686.6; DB 14; Length 4003;
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VERSION	AR454709.1	GI:42688213				
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SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 3708)					
AUTHORS	Homa, F.L., Wathen, M.W., Hopkins, T.A. and Thomsen, D.R.					
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REFERENCE 1  
AUTHORS Saijo,M., Yasuda,Y., Yabe,H., Kato,S., Suzutani,T., De Clercq,E.,  
Niikura,M., Maeda,A., Kurane,I. and Morikawa,S.  
TITLE Bone marrow transplantation in a child with Wiskott-Aldrich  
syndrome latently infected with acyclovir-resistant (ACVr) herpes  
simplex virus type 1: emergence of foscarnet-resistant virus  
originating from the ACVr virus  
J. Med. Virol. 68, 99-104 (2002)  
REFERENCE 2 (bases 1 to 3708)  
AUTHORS Saijo,M., Yasuda,Y., Kato,S., Suzutani,T., Morikawa,S. and  
Kurane,I.  
TITLE Direct Submission  
JOURNAL Submitted (30-AUG-2001) Masayuki Saijo, National Institute of  
Infectious Diseases, Department of Virology 1; 4-7-1 Gakuen,  
Musashimurayama, Tokyo 208-0011, Japan (E-mail:msaijo@nih.go.jp,  
Tel:81-42-561-0771(ex.791), Fax:81-42-564-4881)  
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Db	2332	CTGGGAGCTG	GTGCGCATTCG	GAAGCAGATCGCTCG	CGGATCCCCGAGCAGCCCC	2391
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Qy	2461	TACGGGTTCA	CCGGGGCGAC	ACGTCCTTCGCTCTG	CACTGAGTGGCGCCGACCGGTG	2520
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Qy	2521	ACGACCATCG	CGCGAGATGCT	CTCTCGACAGCGCG	CGTACGTGACGCGCTGGCGG	2580
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Qy	2581	GAGTTCGATC	AGTGTGGCGACT	TTTCCGAGCGCGCCG	CGCATGCGCCCCCGGTCG	2640
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Db	2632	TATTTCAT	GCGCATCATCTA	CGGGGACACG	CACTTTTGGTTTTGTCGCGGCGCTC	2691
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[illegible]

## RESULT 12.

AB070848

# ABO / O LOCUS

## FOCUS DEFINITION

AB070848 3708 bp DNA linear VRL 03-AUG-2002  
Human herpesvirus 1 gene for DNA polymerase, complete cds,  
clone:HSV-1 R98/3.

AB070848  
AB070848.2 GI:18307583  
Human herpesvirus 1  
Human herpesvirus 1  
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
Alphaherpesvirinae; Simplexvirus.  
1  
Saijo, M., Yasuda, Y., Yabe, H., Kato, S., Suzutani, T., De Clercq, E.,  
Niikura, M., Maeda, A., Kurane, I. and Morikawa, S.  
Bone marrow transplantation in a child with Wiskott-Aldrich  
syndrome latently infected with acyclovir-resistant (ACVr) herpes  
simplex virus type 1: emergence of foscarnet-resistant virus  
originating from the ACVr virus  
J. Med. Virol. 68, 99-104 (2002)  
2 (bases 1 to 3708)  
Saijo, M., Yasuda, Y., Kato, S., Suzutani, T., Morikawa, S. and  
Kurane, I.  
Direct Submission  
Submitted (30-AUG-2001) Masayuki Saijo, National Institute of  
Infectious Diseases, Department of Virology 1; 4-7-1 Gakuen,  
Mutsashimurayama, Tokyo 208-0011, Japan (E-mail: masaijo@nih.go.jp,  
Tel: 81-42-561-0771 (ex. 791), Fax: 81-42-564-4881)  
On Jan 23, 2002 this sequence version replaced gi:15408591.  
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Query Match 82.3%; Score 3058.2; DB 14; Length 3708;  
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Qy 61 TCTGGGTTTTTGTGCGCGGACACACCCCGGGGAGCCACCCAGACGGCAGCGCCGCTTGC 120

Db 61 TCGGGTTTTTGTGCGCGCGGCGCTTCGCGGAGCGCGCC--GGGACCCCGGCTTGT 117  
Qy 121 CGCGCGGAGAACTTCTACAACCCCGGCTGCTCAGACCGGAGAAAGGAGGCGGCCCC 180  
Db 118 TTGAGGCAAACTTTTACAAACCCCGGCTGCTGCGGAGCGCAACAGAGCCGAC 177  
Qy 181 GGGCGGCTCAGCGCCCTAGCTACTACAGCGAGTGCAGCAATTTTCAGATTTATCGCCCG 240  
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Qy 301 CGGCGGCGCTTAAGGTGTACTCGGCGGGGAGCAGCGCGAGCTCTCTCGGCTGGGCGG 360  
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Qy	2341	CTCGCGACTGGCTGGCCATGCGAAAGCAGATCCGCTCGCGATCCCCAGAGCAACCC	2400
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Qy	2401	GAGAGGCGCTCTCTCTCGACAAGCAAGCGCGCCATCAAGGTGCTGTGTGCAACTCGGTG	2460
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Qy	2461	TACGGGTTACCGGGGCGAGCAGCGTCTTCTGSCCTGCTGCACTGCGCGCACCGCTG	2520
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Db	2512	ACGACCATCGGCGCGAGATGTCTCTCGGACGCGCGAGTACGTCCACGCGCTCGGGG	2571
Qy	2581	GAGTTCGATCAGCTGTGCGCCGACTTTCGAGGCGCGCGGATGCGCGCCCCCGGTCCG	2640
Db	2572	GCCTTGAAACAGCTCTCTGCGCGATTTCCGAGGCGCGCGACATGCGCGCCCCCGGGCC	2631
Qy	2641	TACTCCATCGCATCATCTACGGGGACAGGGACTCCATTTTCGTTTTGTGCGCGGCTC	2700
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Db	2992	TGGTGGCGGACCCCTGCCCCGAGGGACTGCGAGGCGTTTGGGGCGTCTCTGTAGAGCC	3051
Qy	3061	CATCGGCGCATACCGACCGGAGAGGGAATCCAGACCTTGTCTCTCACCGCGCGAACTG	3120
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Qy	721	TTCCGGCGCATCTCCGGGACCACTTCGAGCGGAGGTGTGAGCGCGCGGACGTGTAC	780	Qy	1801	GCGCTCGCGCGCTGGCGGGCATCAACATCACCGGCACCATCTACGACGCGCAGCAGATC	1860
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Qy	781	TATTTAGAAACGGCGCGACCTGTACTACCGGCTCTTCTGTGGAAAGCGGCGCGGCTG	840	Qy	1861	CGGCTCTTACGTCCTCTGCGCTTGGCGGCGAAGGGCTTCACTCTGCCGAGACCC	1920
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Qy	841	GCCTACTGTGCGACAACCTTTTGGCCCGCGCATACAGGAAGTACGAGGGGGCGTCGAGCC	900	Qy	1921	CAGGGCGGTTTTTCGGGGCTTCGACAAAGGAGGGCCCAAGCGCCGCGCTGCTCGGGG	1980
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Qy	901	ACCACCGGTTTATCTTGGACAACCCCGGGTTTTGTCACTTTCGCTGGTACCGCTCAAG	960	Qy	1981	GAAAGGGAGCGGCGGGGACCGGGAACGGGGACGAGGATAAGGACGACGAGGACGAG	2040
Db	1478	ACACCCGGTTTATCTTGGACAACCCCGGGTTTTGTCACTTTCGCTGGTACCGCTCAAG	1537	Db	2558	GACGAGGAGCGGCCAGAGGAGGAGGGGAGGAGCG-----AGGACGAAACGAGGAGGGC	2611
Qy	961	CCGGCGCGGGAAACGCGCGGCCCAAACCGGCCCCCGACCGGCTTCGGAAACCTCGAGC	1020	Qy	2041	GACGGGACGAGCGCGAGGAGGTGCGCGCGAGACCGGGGGCCGCGACCTTGGGTACCG	2100
Db	1538	CCGGCGCGGAACAACACGCTAGCCACGCGCGGCCCCCGATGGCTTCGGGACATCCAGC	1597	Db	2612	GGGGGCGAGCGGGAGCGCGGGCGGGAGACCGCGCGCGGACCGTGGGGTACCAA	2671
Qy	1021	GACGTCAGTTTAACTGCAAGCGGCAACCTGCGCGCTCGAGGGGGCCATGTGTGACCTG	1080	Qy	2101	GGGGCCCGGCTCTCGACCCACCTCCGGGTTTCACTCGCTCGACCCGCTGGTGGTGTTCAC	2160
Db	1598	GACGTCAGTTTAACTGTCAGCGGCAACCTTGCCCATCGAGGGGGCATGAGCGACCTA	1657	Db	2672	GGGGCCAGGTCTTGCACCCACTTCGGGTTTCACTGTAACCCGCTGGTGGTGTTCGAC	2731
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Qy	1201	GACCTGTCCACCGCCCTCGAGCACTCTCTGTTTTCTGCTCGCATCTCTGCGACCTC	1260	Qy	2281	GGGGCGCGACGCGTGTCTTCGTGAAGGCCACCTAGCGAGAGCTCTGTGAGCATCTCTG	2340
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Qy	1321	TTTGACAGCGAATTCGAGATGCTGCTGCGCTTCAATGACCTTCTGTCAGAGTACGGCCCC	1380	Qy	2401	GAGGAGCGCTCTCTCGACAGCAACGAGCGCGCCCATCAAGGTGGTGTGCAACTCGGTG	2460
Db	1898	TTTGACAGCGAATTCGAGATGCTGCTGCGCTTCAATGACCTTCTGTCAGAGTACGGCCCC	1957	Db	2972	GAGGAGCGCTGCTCTCTGGAACGAGAGCGGCGCCCATCAAGGTGGTGTGTAATCGGTG	3031
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Qy	1441	ACGAGATCTCAAGGTTCCGCTCGAGGGTACGGGGCATGAACGGCGGGGTGTGTTTC	1500	Qy	2521	ACGACCATCGGCGCGAGATGCTCTCTCGGACGCGGGCGGTGTCGACGCGCGCTGGGCG	2580
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Qy	1501	CGCGTGTGGGACATCGGCGAGGCACTTTCAGAAAGCGGACGAAAGATCAAGGTGAACGGG	1560	Qy	2581	GAGTTTCGATCAGCTTCTGCGGCGGCTTTCGCGAGCGCGCGGCTGCGCGCCCCCGGTCCG	2640
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Qy	1561	ATGGTGAACATCGACATGTCGCGCATCATCACCCAGAGGTCAAACTCTCCAGCTACAAG	1620	Qy	2641	TACTTCATGCGCATCATCTACGCGGACACGGAATCCATAATTTGTGCTGTGCGCGGCTC	2700
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DEFINITION	Sequence 7 from patent US 6682892.		
ACCESSION	AR454710		
			PAT 20-FEB-2004

VERSION	AR454710.1	GI:42688214
KEYWORDS	Unknown.	Unknown.
SOURCE	Unknown.	Unknown.
ORGANISM	Unclassified.	Unclassified.
REFERENCE	1 (bases 1 to 3708)	
AUTHORS	Homa,F.L., Wathen,M.W., Hopkins,T.A. and Thomsen,D.R.	
TITLE	Method for treating herpes viruses	
JOURNAL	Patent: US 6682892-A 7 27-JAN-2004;	
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QY	361	GAGGGCTTCGCGCGCGTCCGCTTGCGCCCTGTCGGGCGGTGCGGACCATCGCCCCAAGGG 420
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SEQUENCE from Patent WO2006513.  
DEFINITION AX358316  
ACCESSION AX358316  
VERSION AX358316.1 GI:18674963  
KEYWORDS  
SOURCE  
ORGANISM

Herpes simplex virus (type 1 / strain F)  
Herpes simplex virus (type 1 / strain F)  
Virus; dsDNA viruses, no RNA stage; Herpesviridae;  
Alphan herpesvirinae; Simplexvirus

1  
Homa, F.L., Wathen, M.W., Hopkins, T.A., and Thomsen, D.R.  
A method for treating herpes viruses

PATENT: WO 0206513-A 7 24-JAN-2002  
PHARMACIA & UPJOHN COMPANY (US)

Location/Qualifiers  
1. 3708

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
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ORIGIN

Query Match 82.1%; Score 3053.4; DB 6; Length 3708;  
Best Local Similarity 89.2%; Pred. No. 0;  
Matches 3317; Conservative 0; Mismatches 391; Indels 9; Gaps 2;  
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